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NKX3.1 Genotype and IGF-1 Interact in Prostate Cancer Risk

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14. ABSTRACT

NKX3.1 is a prostate-specific homeobox gene that maps to chromosome 8p21, the most frequ ent target for loss of heterozygosit y in prostate cancer. NKX3.1 is a haploin sufficient tumor supp ressor in the prostate. We found tha t IGFBP-3expreession was activated 10 -fold by NKX3.1 in cell lines and tissues. IGFBP-3 is an inhibito r of IGF -1, a serum c omponent that when ele vated is a risk facto r for prostate cancer. NKX3.1 expression inhibits IGFIR signaling and diminishes IRS -1 phosphorylation. Kn ock down o f IGFBP-3 attenuates the growth suppressive effects of NKX3.1. *NKX3.1* C154T is a poly morphic allele present in ~10% of th e population. The polymorphic allele codes for a variant protei n that replaces arginine 52 with cyst eine. *NXK3.1* C154T co nfers a minimally inc reased risk for prost atic enlargement and for prostate cancer. In a cohort of cases and controls with known *NKX3.1* genotype we found that the effect of serum IGF-1 on prostate cancer risk was seen only in men with at least one polymorphic *NKX3.1* allele. Consistent wi th its apparent inter action with IGF -1 in prostate cancer risk , NKX3.1 R52C protein is attenuated in activation of IGFBP -3. The data therefore show that the two pr ostate cancer risk factors, NKX3.1 R52C and circulating IGF-1 interact. NKX3.1 R52C activates less IGFBP-3 expression than its wild type counterpart and thereby predisposes prostate epithelial cells to the proliferative and antiapoptotic effects of IGF-1, increasing the risk for prostate cancer.

15. SUBJECT TERMS
Prostate cancer, NKX3.1, IGF-1, IGFBP-3,

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INTRODUCTION:

The *NKX3.1* gene is not subject to somatic mutation in prostate cancer (1, 2). Gene targeting studies in mice showed that *Nkx3.1* haploinsufficiency can predispose to prostate epithelial dysplasia and can cooperate with other oncogenic mutations to augment prostate carcinogenesis (3, 4). In gene-targeted mice haploinsufficiency of *Nkx3.1* is accompanied by decreased expression of genes under the regulation of the *Nkx3.l* homeoprotein (5). We have shown that diminished levels of *NKX3.1* expression in primary human prostate cancer and intraepithelial neoplasia correlated with the degree of gene inactivation by deletion, methylation, or both. There is now convincing evidence that *NKX3.1* is both a suppressor protein and is inactivated at the earliest stages of human prostate cancer. NKX3.1 binds to DNA and suppresses expression of genes downstream from cognate DNA binding sites (6). We have yet to identify a promoter that is transcriptionally activated by direct binding of NXK3.1 to its cognate DNA –TAAGTA- sequence. In fact, our experiments with reporter constructs containing NKX3.1 binding DNA suggest that NKX3.1 alone cannot initiate assembly of a transcriptional complex (6). NKX3.1 is known to interact with other transcription factors such as serum response factor (SRF) and serves as a synergistic co activator of promoters with serum response elements such as smooth muscle γ-actin (7). We have sought to identify down stream transcription targets of NKX3.1 in order to understand the tumor suppressor properties of this transcription factor. This project is designed to characterize NKX3.1 activation of IGFBP-3, a known growth suppressor and down regulator of IGF-1 interaction with its receptor.

Task 1. Determine IGFBP-3 expression in prostate specimens from men with different NKX3.1 genotype. Months 1-18

1. *Establish baseline criteria for analysis of tissue microarrays from the Dana Farber- Harvard Prostate SPORE.*
2. *Analyze 40 specimens from Physicians Health Study, known to contain at least one NKX3.1 C154T allele for IGFBP-3, keratin, NKX3.1 and histone expression.*
3. *Analyze specimens with known NKX3.1 homozygous wild type genotype for IGFBP-3, keratin, NKX3.1 and histone expression by quantitative confocal immunomicroscopy.*

We have completed blinded analysis of expression of IGFBP-3 in tissues from the PHS. We received prostatectomy samples from the Physicians Health Study. 33 samples were from patients with *NKX3.1(C154T)* heterozygous and 18 homozygous for wild type NKX3.1. In regions of nonmalignant prostate epithelium IGFBP-3 and cytokeratin were measured by quantitative confocal microscopy (8). Data are shown graphically in Figure 1. The average ratio for specimens with wild type NKX3.1 was 0.98 and for specimens with one variant *NKX3.1* allele was 1.46. The difference between the two was highly statistically significant. Our hypothesis that *NKX3.1* genotype influenced tissue IGFBP-3 levels was not confirmed by these measurements as the relationship between genotype and IGFBP-3 levels was the opposite of what we had

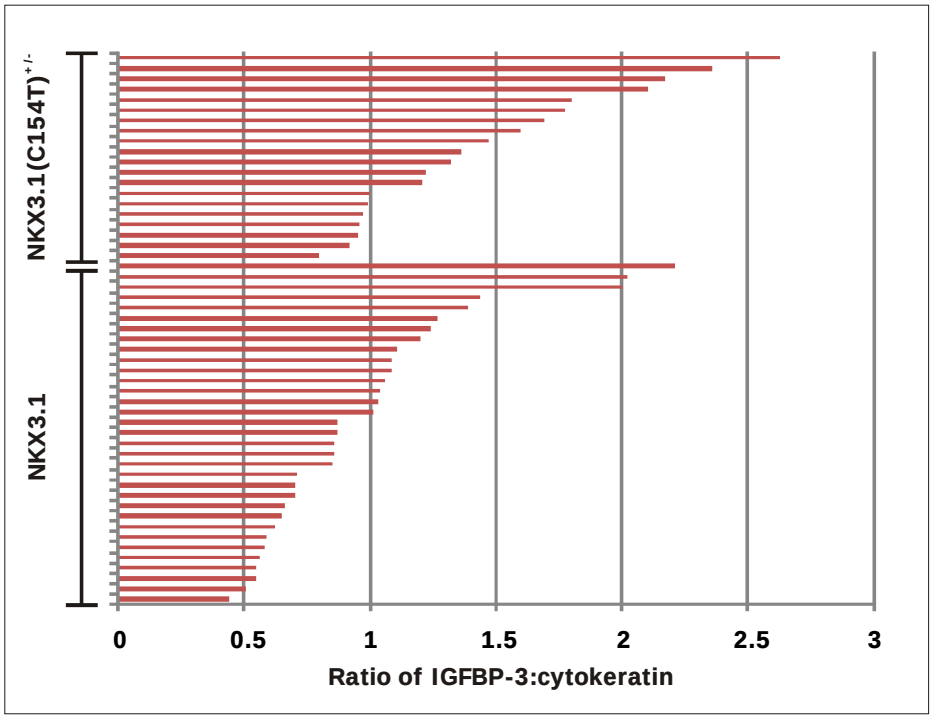


Fig 1. Ratios of IGFBP-3:cytokeratin expression in individual prostatectomy specimens.

predicted. In this sample set IGFBP-3 levels were lower in the wild type than in the variant tissues. Our in vitro and preclinical data do not contain results that explain this result.

Task 2. Analyze serum IGF-1 and IGFBP-3 levels from a cohort of prostate cancer cases and controls that have been genotyped for NKX3.1.

Months 1-18

1. *Identify and aliquot sera from Australian case-control study of men with prostate cancer.*
2. *Batch and send samples to McGill University, Montreal, Canada.*
3. *Test samples and controls for IGF-1 with ELISA assay.*
4. *Statistical analysis of samples for correlation with NKX3.1 genotype at Columbia University.*

We showed that NKX3.1(R52C) and a protein engineered for loss of the serine 48 phosphorylation site NKX3.1(S48A) do not activate expression of IGFBP-3. Consistent with this loss of function we hypothesize that the presence of the variant NKX3.1 protein may interact with circulating serum IGF-I to affect prostate cancer risk. Determination of *NKX3.1* genotype in two populations and analysis of serum IGF-I in the same study subjects is shown.

Study Cohorts. Physicians Health Study: The participants of the Physicians Health Study who comprised the prostate cancer cases and controls have been previously described in papers describing the effect of serum IGF-I (9) and *NKX3.1* genotype (10) on prostate cancer risk. The current analysis includes 673 cases and 527 controls, using a prospective nested case control design. Of the cases, 398 had Gleason score < 7, 257 had Gleason score > 7 = and 18 cases had unknown Gleason scores. Among the cases, 536 were T1/T2 and 101 were locally advanced or metastatic at presentation with the remaining 36 cases of unknown stage. Median age of cases at diagnosis was 70 years.

Risk Factors for Prostate Cancer Study: The Risk Factors for Prostate Cancer Study (RFPCS) is a population-based case-control study of prostate cancer. Prior approval of the study protocol was obtained from all relevant hospital and cancer registry human research ethics committees in Melbourne and Perth. Eligible cases comprised male residents of Melbourne and Perth diagnosed between 1994 and 1997 and recorded in the population-based cancer registries with a histopathology-confirmed diagnosis of adenocarcinoma of the prostate (International Classification of Diseases, 9th revision, rubric 185), excluding well-differentiated tumors (defined as low grade, *i.e.*, those with Gleason scores <5). Cases had to be <70 years of age at diagnosis. Controls were randomly selected from men on the current state electoral rolls and were frequency matched to the predicted age distribution of the cases in a ratio of one control per case. Potential controls were matched against the cancer registries at the time of recruitment to exclude men with a known history of prostate cancer. Controls were identified and interviewed contemporaneously with the cases over the period 1994 to 1997. The cohort is comprised > 95% of Caucasians. The lack of racial diversity is not critical to this analysis since the frequency of the *NKX3.1* polymorphism does not vary between races (10). A total of 798 cases and 527 controls were analyzed. Of the total cases 582 were described as moderate grade and 216 as high grade (Gleason score > 7 or poorly differentiated or undifferentiated tumors). Among the cases 545 were T1/T2 and 249 were locally advanced or metastatic at presentation with the remaining 4 cases of unknown stage. Median age for cases and controls was 62 years Serum IGF-I levels were determined by ELISA using reagents from Diagnostic Systems. All assays were performed in the laboratory of Michael Pollak.

Previously we had shown that among 1253 cases and controls in the PHS *NKX3.1*(C154T) (rs2228013) that codes for NKX3.1(R52C) was a mild risk factor for prostate cancer (10). We expanded this sample set to include cases from the PHS diagnosed more recently so that we now analyzed *NKX3.1* genotypes from 937 prostate cancer cases and 1087 age-matched controls. In this expanded sample set the *NKX3.1*(C154T) allele was related to prostate cancer risk to a similar degree as we had previously published (10) (Table 1). Importantly, among men with prostate cancer diagnosed before age 70, the median age at diagnosis in the PHS, rs2228013 was significantly associated with higher risk of overall prostate cancer (RR=1.55; 95% CI: 1.04-2.31), Gleason <7 (RR=1.71; 95% CI: 1.10-2.65), stage T1/T2 (RR=1.67; 95% CI:

1.09-2.57), and a higher risk of lethal cancer (metastatic cancer at diagnosis or fatal cancer during follow-up (RR=2.15; 95% CI: 1.00-4.63) (Table 2).

Table 1
Odds ratios of Prostate Cancer by NKX3.1 Genotype in the PHS

	Genotype	Case (n)	Case (%)	Control (n)	Control (%)	Odds ratio
Overall	C C	844	90.1	998	91.9	1.00
	C T	91	9.7	84	7.7	
	T T	2	0.2	4	0.4	
	C T/T T	93	9.9	88	8.1	1.25 (0.92-1.71)
Dx 1982-1993	C C	481	90.4	998	91.9	1.00
	C T/T T	51	9.6	88	8.1	1.21 (0.83-1.77)
Dx 1994-2007	C C	363	89.6	998	91.9	1.00
	C T/T T	42	10.4	88	8.1	1.22 (0.77-1.94)

Since NKX3.1 regulates IGFBP-3 expression and IGFBP-3 regulates IGF-I signaling we asked whether *NKX3.1* genotype influenced the effect of IGF-I on prostate cancer risk. From participants in the Physicians Health Study we analyzed 673 prostate cancer cases and 527 matched controls for which we were able to determine both *NKX3.1* genotype and serum levels of IGF-I (Table 3). The majority of cases (69%) in this cohort had been ascertained prior to 1994 and thus had been diagnosed prior to the widespread use of serum PSA for prostate cancer screening. Moreover, the blood samples were collected in 1982, prior to the diagnosis of prostate cancer in the cases. The frequency of rs2228013 among the control participants with IGF-I data was 6.83%, somewhat lower than the overall PHS controls (8.10%), and lower than the 11% we had originally found in our previous study (10). Table 4 shows the frequency of cases and controls displayed by *NKX3.1* genotype and distributed across three tertiles of plasma IGF-I levels. Among participants homozygous for wild type *NKX3.1* there was no effect of plasma IGF-I on prostate cancer occurrence. However, among participants with *NKX3.1*(C154T) we found a 2.5-fold higher risk of prostate cancer comparing the highest to the lowest tertile of plasma IGF-I levels. The positive trend was apparent only among prostate cancer cases diagnosed before 1993, but not among cases diagnosed 1994 and after. *NKX3.1* genotype and serum IGF-I levels did not have a statistically significant interaction even among this subset (p for interaction = 0.2673).

We analyzed *NKX3.1* genotype and serum IGF-I in a second group of cases and controls from the Risk Factors for Prostate Cancer Study conduct by the Victoria Cancer Council in Australia. These cases were diagnosed between 1994 and 1997 and are therefore considered largely screen-detected. The characteristics of this population are shown in the right column of Table 3. In this population rs2228013 was present in 10.4% of the participants. These screened cases had a trend toward a younger age of diagnosis, lower stage distribution and lower grade distribution than the PHS cohort. Among these participants there was no effect of *NKX3.1* genotype on prostate cancer risk. There was also no interaction with levels of serum IGF-I (Table 5). However, the effect of serum IGF-I levels alone on prostate cancer risk was seen in this population.

Table 2
Odds ratios of Prostate Cancer by NKX3.1 Genotype Among Men With Age<70 yrs at Diagnosis: results from the PHS

	Genotype	Cases	(%)	Controls	(%)	Odds ratio
Overall	C C	460	88.3	564	92.2	1.00
	C T/T T	61	11.7	48	7.8	1.55 (1.04-2.31)
Gleason<7	C C	296	86.8	564	92.2	1.00
	C T/T T	45	13.2	48	7.8	1.71 (1.10-2.65)
Gleason≥7	C C	156	91.2	564	92.2	1.00
	C T/T T	15	8.8	48	7.8	1.14 (0.62-2.10)
Stage T1/T2	C C	324	87.3	564	92.2	1.00
	C T/T T	47	12.7	48	7.8	1.67 (1.09-2.57)
Stage T3/T4/N1/M1	C C	110	91.7	564	92.2	1.00
	C T/T T	10	8.3	48	7.8	1.12 (0.54-2.29)
Metastatic or fatal PCa	C C	62	86.1	564	92.2	1.00
	C T/T T	10	13.9	48	7.8	2.15 (1.00-4.63)
Dx year 1982-1993	C C	259	90.2	564	92.2	1.00
	C T/T T	28	9.8	48	7.8	1.30 (0.78-2.19)
Dx year 1994-2007	C C	201	85.9	564	92.2	1.00
	C T/T T	33	14.1	48	7.8	1.80 (1.03-3.15)

Table 3
Characteristics of Two Study Populations for NKX3.1 and IGF-I

		PHS (overall)	PHS (with IGF-I)	RFPCS
Participants		2023	1200	1325
Cases		937	673	798
	Dx prior to 1994	532(56.78)	465(69.09)	0
	Dx after 1994	405(43.22)	208(30.91)	798
Age at Diagnosis				
	<55	21(2.24)	17(2.53)	110 (13.8%)
	55-64	258(27.53)	204(30.31)	421 (52.8%)
	65-69	242(25.83)	169(25.11)	267 (33.5%)
	70-74 ≥ 75	221(23.59) 195(20.81)	160(23.77) 123(18.28)	
Stage				
	T1/T2	647(69.05)	461(68.50)	545 (68.3%)
	T3/T4 N1/M1	150(16.01) 47(5.02)	114(16.94) 39(5.79)	249 (31.2%)
	Missing	93(9.93)	59 (8.77)	4 (0.5%)
Grade				
	Gleason<7,Low/Med Grade	580(61.90)	414(61.52)	582 (72.9%)
	Gleason≥7, High Grade	334(35.64)	239 (35.51)	216 (27.1%)
	Missing	23(2.45)	20(2.97)	
NKX3.1 codon 154	C/C	844	604	719 (90.1%)
	C/T or T/T	93(9.92)	69 (10.25%)	79 (9.9%)

*There was a single determination of 21.57pmole/ml.

Table 4
Odds ratios of Prostate Cancer by NKX3.1 Genotype and IGF-I Level in the Physicians Health Study*

Genotype	IGF-I	Case/ Control	Odds ratio*	p-interaction
Overall: CC	T1**	197/ 162	1.00 (ref)	0.24
	T2	203/ 166	1.029 (0.77-1.38)	
	T3	204/ 163	1.07 (0.79-1.45)	
C/T or T/T	T1	12/ 12	0.82 (0.36-1.87)	
	T2	25/ 11	1.93 (0.92-4.05)	
	T3	32/ 13	2.04 (1.03-4.04)	
Dx 1982-1993: CC	T1	135/ 162	1.00 (ref.)	0.27
	T2	144/ 166	1.23 (0.87-1.73)	
	T3	140/ 163	1.31 (0.92-1.85)	
C/T or T/T	T1	9/ 12	0.98 (0.38-2.55)	
	T2	14/ 11	1.63 (0.70-3.83)	
	T3	23/ 13	2.49 (1.16-5.32)	
Dx 1993-2007: CC	T1	62/ 162	1.00 (ref)	0.57
	T2	59/ 166	0.56 (0.34-0.93)	
	T3	64/ 163	0.69 (0.42-1.14)	
C/T or T/T	T1	3/ 12	0.39 (0.09-1.65)	
	T2	11/ 11	2.68 (0.96-7.52)	
	T3	9/ 13	0.92 (0.31-2.75)	

Adjusted for baseline age, smoking status, and follow-up duration;
** T – tertile

Table 5
NKX3.1 Genotype and Serum IGF-I Levels in Risk Factors for Prostate Cancer Study Participants

Genotype	IGF-I (teriles)	Case/ Control	Odds ratio*	p-interaction
Overall: CC	T1	216/161	1.00 (ref)	0.18
	T2	200/153	0.97 (0.72 - 1.33)	
	T3	303/154	1.39 (1.04 - 1.87)	
C/T or T/T	T1	25/22	0.76 (0.40 - 1.44)	
	T2	30/17	1.39 (0.72 - 2.69)	
	T3	24/20	0.86 (0.44 - 1.64)	

Task 3. Determine the effect of NKX3.1 on prostate cancer cell growth and survival.

1. *Establishment of PC-3 cells expressing NKX3.1. (Months 1-12) We will establish stable PC-3 transfected cells expressing NKX3.1, NKX3.1(R52C), NKX3.1(S48A), NKX3.1(N174Q), and the expression vector pcDNA3.1.*
2. *Determination of IGFBP-3 expression in derivative PC-3 cells. (Months 6-30). We will determine relative expression of IGFBP-3 in the different PC-3 cell clones by western blotting using β-actin as a control and LNCaP cell extracts as a reference.*
3. *IGFBP-3 mRNA (Months 13-36). We will analyze expression of IGFBP-3 mRNA in stable transfectants and transiently transfected PC-3 cells by real time RT-PCR, similar to our experiments with the mouse prostate tissues, but using primers for the human cDNA. We will analyze the level of IGFBP-3 message in stably transfected clones compared to internal controls of GAPDH and β-actin cDNA.*
4. *Effect of NKX3.1 expression on PC-3 cell growth (Months 12-36). We will assay growth of PC-3 derivative cell clones by MTT and by cell counting to compare doubling times to parental and control transfected cells (with expression vector pcDNA3.1).*
5. *Determine the effect of NKX3.1 expression on PC-3 apoptosis (Months 25-36). We will assay the derivative lines for apoptosis. Apoptosis will be assayed by in-situ end labeling (ISEL) as we have previously published and by immunohistochemical assay for activated caspase-3 and cleaved PARP.*
6. *IGFBP-3 knockdown in PC-3 cells (Months 23-36). We will engineer the expression of NKX3.1 and mutants of NKX3.1 in PC-3 prostate cancer cells to determine the effect of NKX.3.1 on PC-3 cell growth and apoptosis. We will validate these results with transient transfection assays and, if necessary, with conditional expression contracts.*

See response to Task 4 below.

Task 4. Determine the effect of NKX3.1 on IGFR-1 signaling pathways and define the role of IGFBP-3 in the interaction between NKX3.1 and IGFR-1.
Months 19-36.
Assay by western blotting the activation of downstream targets of IGFR-1 and determine the effects of NKX3.1. Targets to be analyzed include:

1. *IGFR-1 phosphorylation will be assayed using monoclonal antibodies specific for insulin receptor that cross-react with IGFR-1 (P-Tyr$^{1135/1136}$).*
2. *IRS-1 is phosphorylated on Y1173 by IGFR-1 and can be assayed by IP-western blotting with antiphosphotyrosine antibody (11) or by Novus antibody to mouse IRS-1(phosphoY1179) that cross reacts with human IRS-1.*
3. *Protein kinase B/AKT is recruited to the cell membrane to PIP3 that results in enzyme activation. We will analyze the effect of the NKX3.1 mutant transgenes and IGFBP-3 siRNA on AKT phosphorylation.*
4. *BAD is a proapoptotic BCL family member that is phosphorylated by AKT on serine 136 and by MAPK cascade at serine 112. We will determine the effects of NKX3.1 and IGFBP-3 siRNA on BAD phosphorylation to examine effects on this component of the intrinsic cell death pathway.*
5. *FOXO1 like other members of the forkhead family of transcription factors is affected by IGFR-1 activation. We will use the antiFOXO1(phosphoserine 256) from Cell Signaling to determine FOXO1 phosphorylation in the NKX3.1 expressing cells before and after IGFBP-3 siRNA treatment.*

Tasks 3 and 4 have been largely completed and the data have been published as:

Muhlbradt, E., Asatiani, E., Ortner, E., Wang, A, and Gelmann, E.P. NKX3.1 activates expression of IGFBP-3 to mediate IGF-I signaling and cell proliferation. *Cancer Research,* 69:2615-22, 2009. The paper wais included as part of the 2008-09 progress report.

Amino acid 52 affected by rs2228013 is an arginine, located in a consensus motif that is a site for phosphorylation at serine 48. Replacement of arginine 52 with cysteine decreases phosphorylation at serine 48 by 70% (10). Thus a missense mutation at serine 48 potentially generates a protein with analogous, but more absolute, loss of serine 48 phosphorylation compared to NXK3.1(R52C). Expression of NKX3.1(R52C) in PC-3 cells induced substantially less *IGFBP-3* mRNA than did wild type NKX3.1 (Figure 1A). The mutant NKX3.1(S48A) protein was also attenuated in *IGFBP-3* induction, perhaps to a greater degree than NKX3.1(R52C) (Figure 1B). Western blotting confirmed that, as expected, neither NKX3.1(R52C) nor NKX3.1(S48A) induced IGFBP-3 protein expression in PC-3 cells (Figure 1C).

NKX3.1 expression attenuated IGFR-I activation in PC-3 cells via induced expression of IGFBP-3. The effect of NKX3.1 on IGFR-I activation was not seen when Long R-IGF-I, an IGFR-I ligand that does not bind to IGFBP-3 was used, or when cells were pretreated with *IGFBP-3* siRNA (12). In contrast, neither NKX3.1(R52C) nor NKX3.1(S48A) had an effect on IGFR-I signaling (Figures 2A and B). Moreover, signaling downstream from IGFR-I to IRS-1 is attenuated by NKX3.1 expression, but not by NKX3.1(R52C) or NKX3.1(S48A) (Figure 2C). NKX3.1 suppresses cell proliferation in culture, an effect that is abrogated by siRNA to *IGFBP-3* (12). PC-3 cells have a doubling time of approximately 24 hrs that is extended to approximately 30 hrs by expression of NKX3.1. Neither NKX3.1(R52C) nor NKX3.1(S48A) affected PC-3 cell doubling time (Table 6) despite levels of NKX3.1 protein expression comparable to levels of wild type protein that suppressed proliferation.

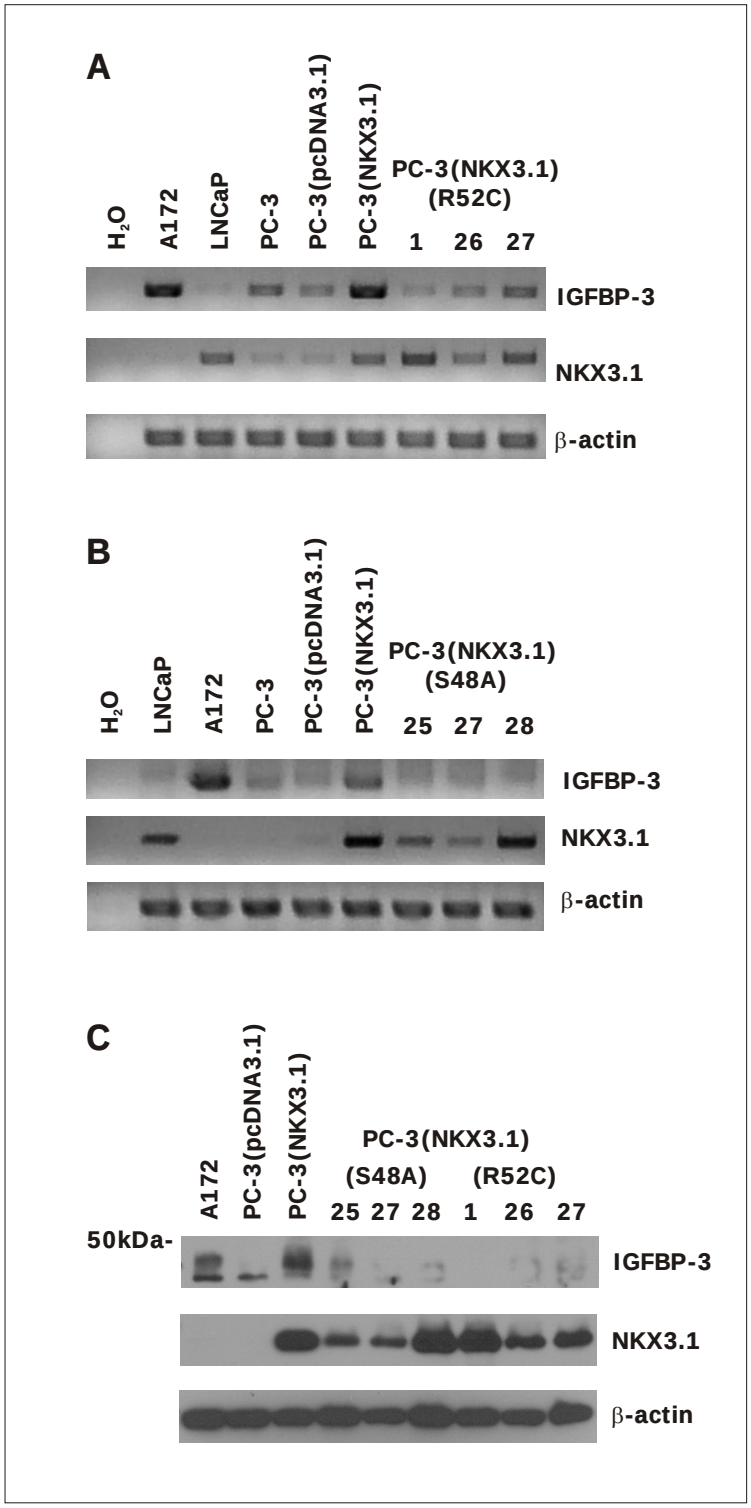
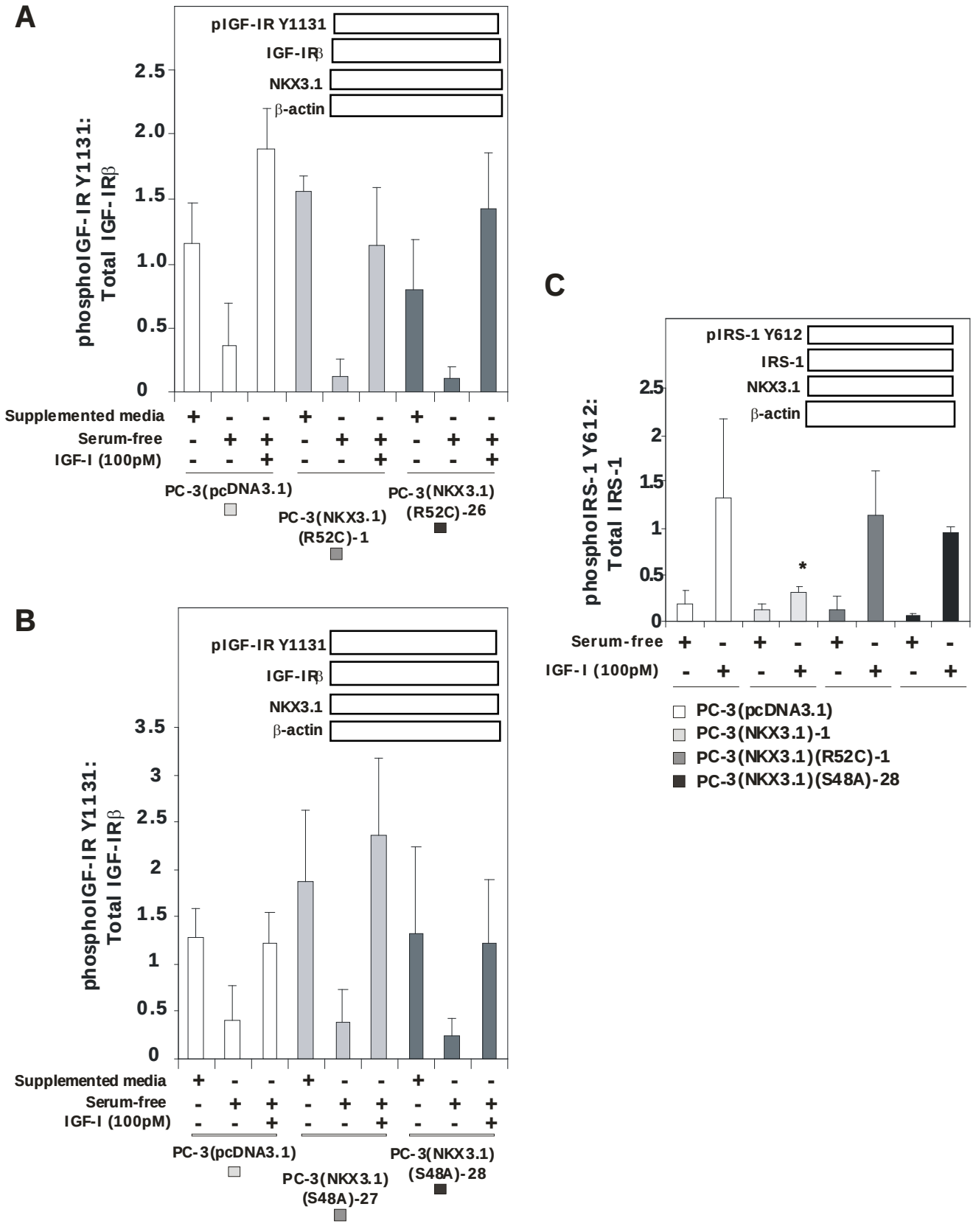


Figure 2. The effect of NKX3.1 variant proteins on IGFBP-3 expression in PC-3 cell clones. A and B. RT-PCR analysis of 250ng total mRNA isolated from PC-3 cell clones. A172 is a positive control for IGFBP-3 mRNA expression and LNCaP is a positive control for NKX3.1 mRNA expression. C. Western blot analysis of 60µg whole cell lysate from PC-3(pcDNA3.1), PC-3(NKX3.1), PC-3(NKX3.1 R52C), and PC-3(NKX3.1 S48A) cell clones. A172 cell line was used as a positive control for IGFBP-3 protein expression.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Serum-free
IGF-I (100pM)
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PC-3(NKX3.1)
(R52C)-1
PC-3(NKX3.1)
(R52C)-26
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pIGF-IR Y1131
IGF-IRβ
NKX3.1
β-actin
phosphoIGF-IR Y1131:
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Serum-free
IGF-I (100pM)
PC-3(pcDNA3.1)
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PC-3(NKX3.1)(R52C)-1
PC-3(NKX3.1)(S48A)-28

Figure 2. The effect of NKX3.1 variant proteins on IGF-IR activation in PC-3 cells. A. Western blot analysis of 90µg of total protein extracted from PC-3(pcDNA3.1) and PC-3(NKX3.1)(R52C) stable cell clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. B. Western blot analysis of 90 µg of total protein extracted from PC-3(pcDNA3.1) and PC-3(NKX3.1)(S48A) stable cell clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. C. Western blot analysis of 90µg of total protein extracted from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, PC-3(NKX3.1)(R52C)-1, and PC-3(NKX3.1)(S48A)-28 clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. * indicates a value different from the PC-3(pcDNA3.1) control with a $p<0.001$.

Table 6
Effect of NKX3.1 Expression on Cell Proliferation

Cell Type	Doubling Time	p-value
PC-3	25.34 ± 1.91	0.1716
PC-3(Control)	24.26 ± 2.05	*
PC-3(NKX3.1)-1	32.24 ± 5.91	0.0037
PC-3(NKX3.1)-2	38.88 ± 7.82	0.0002
PC-3(NKX3.1)-8	30.24 ± 2.55	0.002
PC-3(NKX3.1)(S48A)-25	22.19 ± 1.31	0.1368
PC-3(NKX3.1)(S48A)-27	22.94 ± 0.98	0.3221
PC-3(NKX3.1)(S48A)-28	22.42 ± 2.00	0.2053
PC-3(NKX3.1(R52C)-1	24.34 ± 1.50	0.9555
PC-3(NKX3.1)(R52C)-26	25.94 ± 1.48	0.2264
PC-3(NKX3.1)(R52C)-27	26.41 ± 1.69	0.1357

The cell doubling time, in hours, of parental PC-3 cells, PC-3(pcDNA3.1) cells, and PC-3(NKX3.1) clones was assayed by cell counting. Cells were counted at 24, 48, 72, and 96 hours post-seeding and doubling times were calculated. In the lower section of the table PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells were treated with transfection reagent alone, the missense siRNA oligonucleotide, and the IGFBP-3 siRNA oligonucleotide for 24 hours before the first cell count was taken. p-values were calculated in comparison to the PC-3(pcDNA3.1) cell doubling time, using ANOVA. NS = not significant.

KEY RESEARCH ACCOMPLISHMENTS:

- NKX3.1 activates IGFBP-3
- IGFBP-3 mediates, in part, growth suppression by NKX3.1
- NKX3.1 affects IGF-1 signaling and activation by IGF1-R by activation of IGFBP-3
- NKX3.1 C154T polymorphism does not interact with serum IGF-1 in prostate cancer risk

REPORTABLE OUTCOMES:

Publication:
Muhlbradt, E., Asatiani, E., Ortner, E., Wang, A, and Gelmann, E.P. NKX3.1 activates expression of IGFBP-3 to mediate IGF-I signaling and cell proliferation. *Cancer Research,* 69:2615-22, 2009.

Submitted Manuscript:
Erin Muhlbradt, Jing Ma, Gianluca Severi, Elizabeth Ortner, Vanessa Hayes, Hoa N. Hoang, Meir Stampfer, Graham Giles, Michael Pollak, and Edward P. Gelmann. Variant NKX3.1 and serum IGF-1 – investigation of interaction in prostate cancer. Submitted to *Cancer Epidemiology, Biomarkers, and Prevention.*

Employment

Erin Muhlbradt, graduate student who participated in this project
Hired as Bioinformatics Research Analyst, Northrup-Grumman. Reston, VA

CONCLUSION: This project is completed and has achieved its goals. Our experimental studies have shown that NKX3.1 activates IGFBP-3 expression and that IGFBP-3 mediates to a large degree the growth suppressive effects of NKX3.1 in vitro. The mechanism of this is via interference with the IGF-1 stimulation of the IGF-1R. The variant NKX3.1 coded by the polymorphic locus *NKX3.1* C154T is attenuated in IGFBP-3 activation and growth suppression in vitro. *NKX3.1* C154T is a genetic determinant that is a mild risk factor for prostate cancer. However in our study we did not confirm that *NKX3.*1 genotype sensitizes men to procarcinogenesis in the prostate by circulating IGF-1. A second paper is being drafted now to complete the formal literature report of our data.

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Appendices

Muhlbradt, E., Asatiani, E., Ortner, E., Wang, A, and Gelmann, E.P. NKX3.1 activates expression of IGFBP-3 to mediate IGF-I signaling and cell proliferation. *Cancer Research,* 69:2615-22, 2009.

Erin Muhlbradt, Jing Ma, Gianluca Severi, Elizabeth Ortner, Vanessa Hayes, Hoa N. Hoang, Meir Stampfer, Graham Giles, Michael Pollak, and Edward P. Gelmann. Variant NKX3.1 and serum IGF-1 – investigation of interaction in prostate cancer. Submitted to *Cancer Epidemiology, Biomarkers, and Prevention.*

NKX3.1 Activates Expression of Insulin-like Growth Factor Binding Protein-3 to Mediate Insulin-like Growth Factor-I Signaling and Cell Proliferation

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Abstract

***NKX3.1* is a homeobox gene that codes for a haploinsufficient prostate cancer tumor suppressor. NKX3.1 protein levels are down-regulated in the majority of primary prostate cancer tissues. NKX3.1 expression in PC-3 cells increased insulin-like growth factor binding protein-3 (IGFBP-3) mRNA expression 10-fold as determined by expression microarray analysis. In both stably and transiently transfected PC-3 cells and in LNCaP cells, NKX3.1 expression increased IGFBP-3 mRNA and protein expression. In prostates of *Nkx3.1* gene-targeted mice *Igfbp-3* mRNA levels correlated with *Nkx3.1* copy number. NKX3.1 expression in PC-3 cells attenuated the ability of insulin-like growth factor-I (IGF-I) to induce phosphorylation of type I IGF receptor (IGF-IR), insulin receptor substrate 1, phosphatidylinositol 3-kinase, and AKT. The effect of NKX3.1 on IGF-I signaling was not seen when cells were exposed to long-R3-IGF-I, an IGF-I variant peptide that does not bind to IGFBP-3. Additionally, small interfering RNA–induced knockdown of IGFBP-3 expression partially reversed the attenuation of IGF-IR signaling by NKX3.1 and abrogated NKX3.1 suppression of PC-3 cell proliferation. Thus, there is a close relationship *in vitro* and *in vivo* between NKX3.1 and IGFBP-3. The growth-suppressive effects of NKX3.1 in prostate cells are mediated, in part, by activation of IGFBP-3 expression.** [Cancer Res 2009;69(6):2615–22]

Introduction

Adenocarcinoma of the prostate, like many epithelial malignancies, initiates in luminal epithelial cells in prostatic ducts that acquire the precursor or gatekeeper mutations required for development of the malignant phenotype. Early in prostate cancer, a region of 8p21.2 is lost in the majority of cancers (1). At least one target for 8p21.2 loss is the homeobox gene *NKX3.1*, which is expressed specifically in prostate luminal epithelial cells. NKX3.1 undergoes progressive loss of protein expression during prostate cancer progression from hormone dependence to hormone independence and metastatic disease (2, 3).

The *Nkx3.1* gene is not subject to somatic mutation in prostate cancer (4, 5). Gene targeting studies in mice showed that NKX3.1 haploinsufficiency alone can predispose to prostate epithelial dysplasia and can cooperate with other oncogenic mutations to augment prostate carcinogenesis (6, 7). In gene-targeted mice, decreased Nkx3.1 expression is accompanied by decreased expression of genes under the regulation of the Nkx3.l homeoprotein (8). We have recently shown that diminished levels of NKX3.1 expression in primary human prostate cancer and intraepithelial neoplasia correlated with the degree of gene inactivation by deletion, methylation, or both. Not only is NKX3.1 down-regulated in preinvasive prostate cancer but NKX3.1 expression is also reduced in regions of inflammatory atrophy that are precursors for malignant transformation (9). Inflammatory cytokines in these lesions can induce ubiquitination of NKX3.1 and protein loss (10). Therefore, NKX3.1 may play a role in premalignant events in the prostate gland by modulating gene expression to increase the susceptibility of prostate epithelial cells to malignant transformation. We have sought to characterize the gene expression program activated by NKX3.1 in human cells. Here we show *in vitro* and *in vivo* that NKX3.1 activates expression of insulin-like growth factor binding protein-3 (IGFBP-3), a known growth suppressor protein and down-regulator of insulin-like growth factor-I (IGF-I) activity.

IGFBP-3 is one of six IGFBPs that bind to and modulate the activity of IGFs. IGFBP-3 is a highly abundant serum protein and therefore affects the physiologic bioavailability of circulating IGF-I (11). In the pericellular environment, IGFBP-3 is thought to be proapoptotic and to counteract the proliferative effects of IGF-I (12). Pericellular proteases cleave IGFBP-3, thus releasing IGF-I to bind to the type I IGF receptor (IGF-IR). For example, prostate-specific antigen is a metalloproteinase that cleaves IGFBP-3 to yield at least seven proteolytic fragments, some of which retain the ability to bind IGF-I, albeit with lower affinity than the intact protein (13–16). The interaction of IGFBP-3 with cells is more complex than suggested by its interactions with IGF-I. IGFBP-3 stimulates cells directly as shown by the biological effects of IGFBP-3 mutant proteins that lack IGF-I binding (17). Interestingly, although IGFBP-3 expression was not identified in a high-throughput expression analysis of *Nkx3.1* gene-targeted mice (8), IGFBP-3 was identified as a major target of down-regulation in prostate cancer compared with nonmalignant prostate tissue (18). We now present data showing a role for IGFBP-3 in growth suppression by NKX3.1. We propose that IGFBP-3 expression represents an important mechanistic link between the tumor-suppressive effects of NKX3.1 and the prosurvival and proliferative effects of IGF-I, a peptide growth factor that has been implicated in prostate carcinogenesis.

Materials and Methods

Expression array analysis. Total RNA from stable PC-3(NKX3.1) and PC-3(pcDNA3.1) cells was harvested using the RNeasy Miniprep kit (Qiagen, Inc.). First-strand cDNA synthesis from total RNA was carried out using the GeneChip T7-Oligo(dT) primer kit (Affymetrix). Second-strand

Note: Supplementary data for this article are available at Cancer Research Online (http://cancerres.aacrjournals.org/).

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cDNA synthesis was done using the SuperScript Choice System (Invitrogen). The cDNA was then processed using the GeneChip Sample Cleanup Module (Affymetrix). Amplification and biotin labeling of antisense cRNA were carried out using the BioArray High Efficiency RNA Transcript Labeling system (Affymetrix). Finally, the GeneChip Sample Cleanup Module (Affymetrix) was used to clean up the biotinylated cRNA before it was sent for analysis on an Affymetrix U-133 array system.

Cell culture and reagents. The prostate cancer cell lines PC-3 and LNCaP and the A172 human glioblastoma cell line were obtained from American Type Culture Collection. PC-3 and A172 cell lines were grown in modified IMEM (Invitrogen) containing 10% fetal bovine serum (FBS). LNCaP cells were grown in modified IMEM with phenol red (Invitrogen) containing 10% FBS. The PC-3 cells stably expressing the NKX3.1 expression vector were continuously grown in modified IMEM (Invitrogen) containing 10% FBS and 1.2 mg/mL G418 (Invitrogen). LNCaP cells were serum starved overnight in IMEM supplemented with 5% charcoal-stripped calf serum and treated with 10 nmol/L R1881 for 48 h before harvesting.

Plasmids and transfection. Full-length NKX3.1 was cloned into the mammalian expression vector pcDNA3.1 (Invitrogen) as previously described (19). The phosphatase and tensin homologue (PTEN) expression vector, cloned into pcDNA3.1, was a kind gift from Charles Sawyers (Memorial Sloan-Kettering Cancer Center, New York, NY; ref. 20). Transient and stable transfections were carried out in 75-cm^2 cell culture flasks (Corning, Inc.). Briefly, PC-3 and LNCaP prostate cancer cells were grown to 40% to 60% confluence, and 4 μg of plasmid DNA were transfected into the cell lines using Lipofectamine Plus reagents (Invitrogen) in Opti-MEM (Invitrogen). After a 4-h incubation, the medium was replaced with IMEM containing 10% FBS for an additional 24 h. The PC-3 clones that stably express NKX3.1 were derived by transfection. After 4-h incubation with transfection reagent, PC-3 cells were trypsinized and seeded at a 1:30 density in Falcon Integrid 20 mm grid tissue culture dishes (Becton Dickinson) in modified IMEM containing 10% FBS and 1.2 mg/mL G418 (Invitrogen). The medium was replaced every 4 d until colonies derived from a single cell could be seen with a light microscope. Single-clone colonies were isolated with sterile cloning discs (Scienceware) soaked in 0.25% trypsin-EDTA (Invitrogen) and grown to confluence in six-well tissue culture dishes (Corning) for further study.

Western blot analysis. Cells were grown to 60% to 80% confluence and medium was aspirated from the tissues culture dish. Immediately following medium aspiration, lysis buffer was pipetted directly onto the cell monolayer and cells were scraped from the tissue culture flask. Cells were lysed with radioimmunoprecipitation assay buffer containing Complete Mini protease inhibitors (Roche) and/or phosphatase inhibitors (Cell Signaling) followed by brief sonication to complete lysis. Sixty to ninety micrograms of total cell lysate were boiled in Novex 2× Tris-glycine SDS sample buffer (Invitrogen) containing β-mercaptoethanol for 6 min and resolved on a 10% to 20% Tris-glycine SDS-PAGE gel (Invitrogen). Protein was then transferred onto a nitrocellulose membrane (Bio-Rad) and probed with primary antibodies at the following concentrations: β-actin (Sigma), 1:10,000; NKX3.1 (ref. 2), 1:2,000; IGFBP-3 (Santa Cruz Biotechnology), 1:8,000; AKT (Cell Signaling), 1:7,500; phospho-AKT Thr308 (Cell Signaling), 1:7,500, at 4°C overnight, followed by three washes in PBST. Horseradish peroxidase–conjugated goat anti-rabbit and goat anti-mouse (ImmunoPure antibodies, Pierce Biotechnology) secondary antibodies in 1% milk or 1% bovine serum albumin were applied for 1 h at room temperature. Signal detection was done with SuperSignal West Pico Chemiluminescent Substrate (Pierce Biotechnology).

Reverse transcription-PCR analysis. Total RNA was extracted using the RNeasy Mini Kit (Qiagen) and cells were homogenized using the Qiashredder (Qiagen) method. RNA (125–250 ng) was added to the reverse transcription-PCR (RT-PCR) master mix from OneStep RT-PCR Kit (Qiagen; includes 5× buffer, deoxynucleotide triphosphates, and Taq polymerase). The following primers were used in the RT-PCR reactions: β-actin (fwd 5′-GGCCACGGCTGCTTC-3′ and rev 5′-GTTGGCGTACAGGTCTTTGC-3′), NKX3.1 (fwd 5′-GCCGCACGAGCAGCCAGAGACA-3′ and rev 5′-TTCAGGG-CCGGCAAAGAGGAGTG-3′), IGFBP-3 (fwd 5′-CGCCAGCTCCAGGAAATG-3′ and rev 5′-GCATGCCCTTTCTTGATGATG-3′), IGFBP-4 (fwd 5′-TTAGCC-CAAGAGGTCTGAGC-3′ and rev 5′-CTGTGCTTCAAGTCTTCCTTTG-3′), and lamin A/C (fwd 5′-AACTTCAGGATGAGATGCTGCG-3′ and rev 5′-GT-CCAGAAGCTCCTGGTACTCGT-3′). RT-PCR was done in a Techne Techgene PCR machine; 30 min at 50°C, 15 min at 94°C, 22 to 30 cycles of 30 s to 1 min at 94°C, 30 s to 1 min at melting temperatures of 55°C to 65°C, and 30 s to 1 min at 72°C, followed by 15 min at 72°C. Samples were stored on ice until and mixed with 10× Blue Juice gel loading buffer (Invitrogen) and run on a 1.5% agarose gel containing 0.1 μg/mL ethidium bromide in Tris-acetate-EDTA buffer. Gels were imaged on a luminometer and recorded using a Kodak one-dimensional digital camera.

Real-time RT-PCR analysis of murine prostate RNA. Frozen anterior prostates from three individual mice of each of genotypes *Nkx3.1*$^{+/+}$, *Nkx3.1*$^{+/-}$, and *Nkx3.1*$^{-/-}$, from both 4- and 12 mo-old animals, were generously provided by Cory Abate-Shen (Columbia University, New York, NY; ref. 6). mRNA was extracted using Qiagen RNeasy mini kit. The real-time quantitative PCR TaqMan assays were done on the ABI PRISM 7700 Sequence Detection System (SDS) equipment (Applied Biosystems). The primers and probe were selected for *igfbp-3* using Primer Express software (Applied Biosystems). The primer sequences were forward, 5′-GCAGG-CAGCCTAAGCACC-3′, and reverse, 5′-CCTCCTCGGACTCACTGAT-3′. The probe sequence (TCCCCTCCCAACCTGCTCCAGG) was labeled at the 5′ end with the reporter molecule 6-carboxyfluorescein (FAM) and at the 3′ with the quencher BHQ-1. Amplification of commercially available endogenous VIC-labeled control, rodent glyceraldehyde-3-phosphate dehydrogenase (GAPDH; Applied Biosystems), was used to standardize the amount of sample DNA added. Dilutions of DNA from the cell line (LNCaP) were used to construct standard curves for the target gene and endogenous control. TaqMan Universal PCR Master Mix was combined with 100 ng of sample DNA, 900 nmol/L final concentration of primers, and 100 nmol/L final concentration of the probe. All samples were analyzed as replicates of four wells. Relative quantitation of the data from 7700 SDS was done using SDS 2.1 Software (Applied Biosystems).

IGF-IR activation and signaling. Cells were plated in 100-mm culture dishes and washed twice with 1× PBS before being serum starved for 14 to 16 h in modified IMEM containing 1.2 mg/mL G418 (Invitrogen). Cells were then washed once with PBS and treated for 3 min with 100 pmol/L IGF-I (a gift from Dr. J. Toretsky, Georgetown University, Washington, DC) or long-R3-IGF-I (GroPep) in IMEM at 37°C. The medium was immediately aspirated and cells were scraped from the flask and suspended in 2× cell lysis buffer (Cell Signaling) containing phosphatase inhibitors and protease inhibitors by using Complete Mini tablets (Roche). Western blot analysis was completed as described above with anti–IGF-IRβ (Cell Signaling), anti–phospho-IGF-IR (Tyr^{1131}) (Cell Signaling), anti–insulin receptor substrate 1 (IRS-1; Upstate), anti–IRS-1[pY^{612}] (Biosource), anti–phosphatidylinositol 3-kinase (PI3K) p85 (Cell Signaling), and anti–phospho-PI3K [pY^{458}] (Cell Signaling) primary antibodies. Bands were quantified by Scion Imager software and P values were assessed from triplicate experiments by t test analysis using Prism GraphPad software (*, $P < 0.05$; **, $P < 0.005$; ***, $P < 0.001$).

Cell proliferation assay. PC-3, PC-3(pcDNA3.1), and PC-3(NKX3.1) cells were seeded in triplicate in 96-well plates at a concentration of 4,000 per well in IMEM containing 10% FBS (PC-3) or 10% FBS plus 1.2 mg/mL G418 [PC-3(pcDNA3.1) and PC-3(NKX3.1)] and incubated for 24 h at 37°C. At 24, 48, 72, and 96 h after seeding, wells were trypsinized, suspended in IMEM, and immediately counted in a Beckman Coulter Z1 cell counter. Doubling times were calculated using Microsoft Excel and P values were calculated by ANOVA.

Tumor xenografts. Animal studies were carried out under the approved protocol AAAA-7422 as per Columbia University Institutional Animal Care and Use Committee guidelines and approval. Cell lines were grown to 80% confluence in IMEM + 10% FBS + 1.2 mg/mL G418 in a Hyperflask (Corning) and trypsinized with 0.25% trypsin-EDTA (Invitrogen). Cells were resuspended in IMEM containing 10% FBS to deactivate trypsin and washed twice with PBS. Cells were then counted and resuspended in PBS at a concentration of 3×10^7/mL. Cell suspensions (150 μL) were injected into 5-wk-old female NCr-Nude mice (Taconic Farms) on their ventral surface

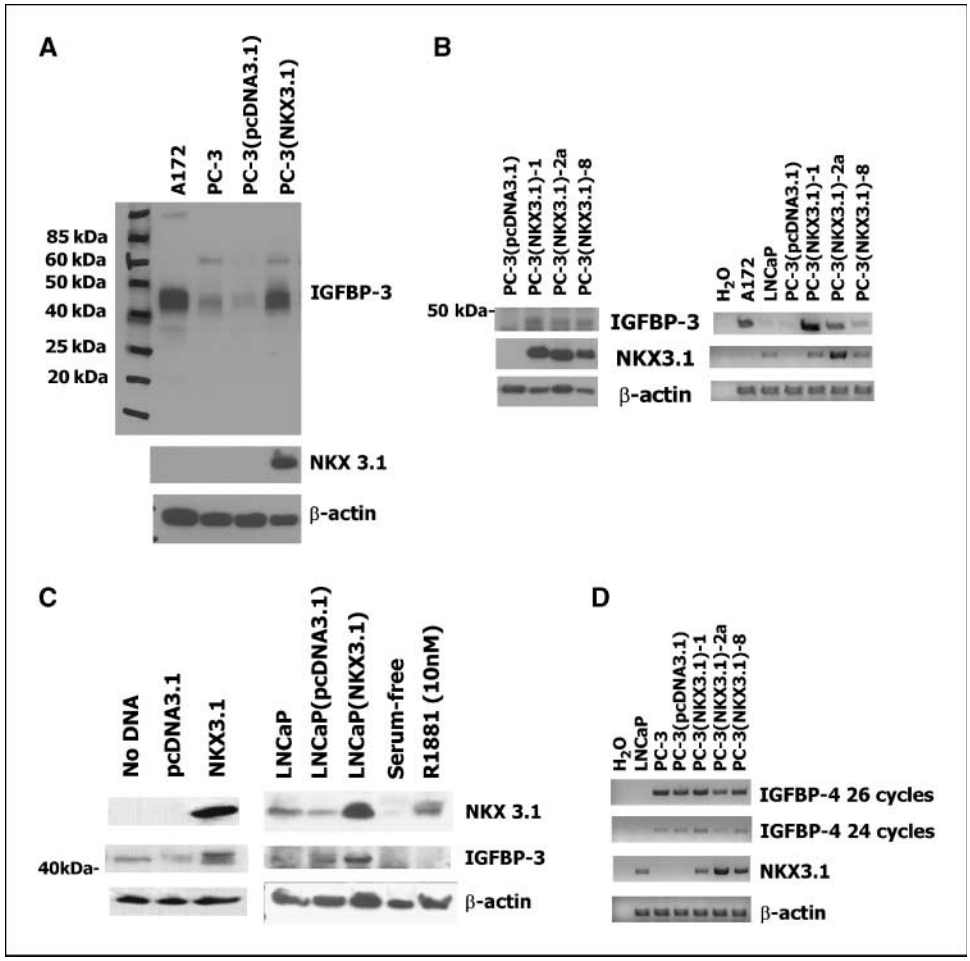

Figure 1. NKX3.1 up-regulates the expression of IGFBP-3 in prostate cancer cell lines. *A,* Western blot analysis of cell extracts from stably expressing PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cell clones that have been analyzed by expression array. *B, left,* Western blot analysis of extracts from additional PC-3 clones expressing NKX3.1. *Right,* RT-PCR analysis of PC-3(pcDNA3.1) and PC-3(NKX3.1) clones for *NKX3.1* and *IGFBP-3* expression. A172 cell extract is a positive control for *IGFBP-3* expression and LNCaP cell extract is used as a positive control for *NKX3.1* expression. *C, left,* Western blot analysis of extracts from PC-3 cells transiently transfected with an NKX3.1 expression vector. *Right,* Western blot analysis of extracts from LNCaP cells transiently transfected with an NKX3.1 expression vector or serum starved in medium supplemented with 5% charcoal-stripped calf serum overnight and treated with 10 nmol/L R1881. *D,* RT-PCR analysis of *IGFBP-4* mRNA expression in PC-3(pcDNA3.1) and PC-3(NKX3.1) clones.

and tumors were measured in two dimensions once a week. We performed 20 inoculations per cell line. All measurements were done by one observer (E.M.). Once the tumors reached 500 mm^3 or if illness was observed, mice were sacrificed and tumors were dissected and stored in 10% buffered formalin for paraffin embedding or in RNA*later* (Qiagen) at −80°C for Western blot analysis.

Immunohistochemistry. Cells grown under tissue culture conditions were embedded in 1% agarose before sectioning and staining. Paraffin embedding and sectioning of the tumor xenografts and agarose cell plugs were done by the Molecular Pathology Shared Resource of the Herbert Irving Comprehensive Cancer Center at Columbia University. Slides were microwaved for 5 min and immersed in two washes of xylene, followed by successive washes in 100%, 90%, and 70% ethanol and then by a 5-min wash in PBS. Slides were immersed in 10 mmol/L citrate buffer at pH 6.0 and steamed in a Black and Decker vegetable steamer for 40 min. Slides were fully cooled to room temperature and washed once with PBS before the blocking step, horse serum in PBS (1:66, Pierce) for 30 min at room temperature. NKX3.1 primary antibody (1:500; Zymed) was applied for 1 h at room temperature followed by biotin antimouse secondary antibody for 30 min (1:200; Vector Laboratories). This was followed by application of Vectastain Elite ABC kit (Vector Laboratories) and Vector VIP substrate kit (Vector Laboratories). Methyl green (Vector Laboratories) was used as a nuclear counterstain.

Small interfering RNA knockdown of IGFBP-3. A series of small interfering RNA (siRNA) oligonucleotides were purchased from Dharmacon. Another siRNA sequence was derived from sequences published by Stewart and colleagues (21): a siRNA duplex directed against nucleotides 603 to 623 of IGFBP-3 mRNA (reference sequence NM_000598; 5′-AAUCAUCAUCAAGAAAGGGCA-3′). Control siRNA sequences included a mismatched oligonucleotide that differed from the IGFBP-3 siRNA oligonucleotide by 1 bp (5′-AAUCAUCUACAAGAAAGGGCA-3′), and the lamin A/C positive control sequence (5′-GGUGGUGACGAUGUGGGCU-3′). This single siRNA sequence was the only one of 11 siRNA sequences tested. The 10 *IGFBP-3* siRNA sequences that had no effect are shown in Supplementary Table S1. Cells (2×10^5) were plated in triplicate in a six-well plate in IMEM + 10% FBS + 1.2 mg/mL G418 the night before the exposure to the oligonucleotides. Cells were transfected with 20 μmol/L of siRNA oligonucleotide using Lipofectamine (Invitrogen) in Opti-MEM (Invitrogen). The medium was changed back to IMEM + 10% FBS + 1.2 mg/mL G418 at 3.5 h posttransfection, and knockdown of IGFBP-3 mRNA was assayed at 24 and 96 h by RT-PCR. In the cell proliferation assay, knockdown was allowed to proceed for 24 h before the initial cell count. For the assessment of IGF-IR activation and downstream signaling, 1×10^6 cells were plated in IMEM + 10% FBS + 1.2 mg/mL G418 the night before exposure to the oligonucleotides. Cells pretreated with oligonucleotide for up to 16 h were washed twice with PBS and serum starved for 14 to 16 h. Cells were further washed with PBS and treated with 100 pmol/L IGF-I for 3 min at 37°C.

Results

Effect of NKX3.1 on gene expression in PC-3 prostate cancer cells. To identify genes whose expression is affected by NKX3.1, we initially generated independently transfected clones of PC-3 prostate cancer cells chosen because PC-3 cells express essentially no NKX3.1 protein and express NKX3.1 mRNA at ~1/250 the level

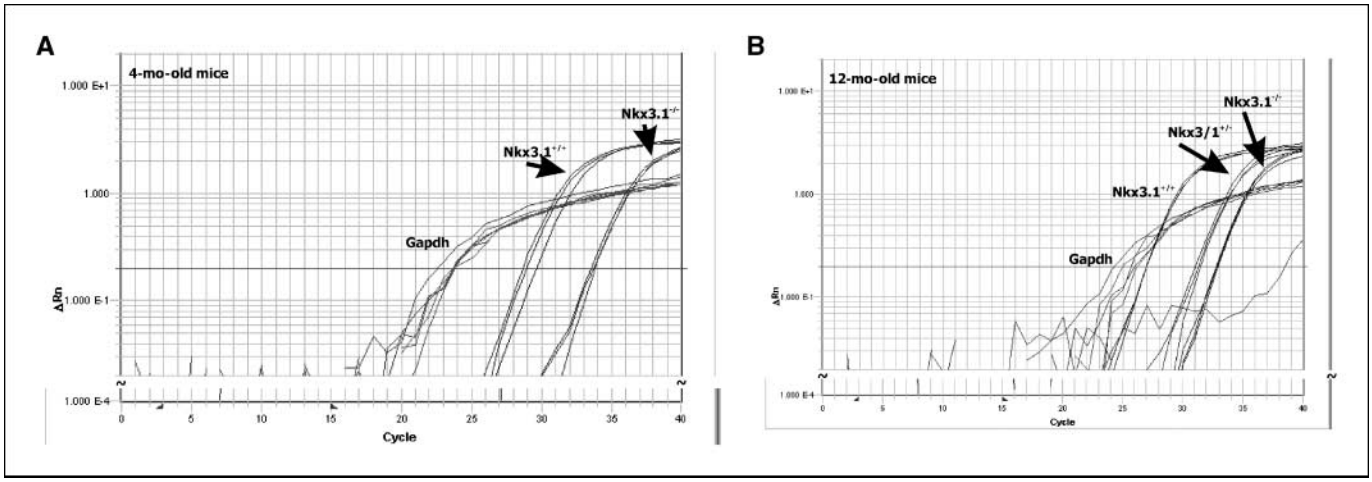

Figure 2. *Nkx3.1* and *Igfbp-3* expression in mouse prostate. Real-time RT-PCR analysis of mRNA extracts of prostatic tissue of *Nkx3.1* gene-targeted mice at 4 mo (*A*) and 12 mo (*B*) of age. Anterior prostates were analyzed from three separate animals of each genotype at each time point. *Gapdh* expression was used as a loading control. Each one of the multiple assay lines in each group represents the results of a single tissue sample. The results correlated with *Nkx3.1* genotype.

seen in LNCaP cells.[3] Two derivative PC-3 cell lines transfected with the pcDNA3.1 empty expression vector and two derivative NKX3.1 expressing clones were analyzed using the Affymetrix U-133 expression arrays. Approximately 99% of the signals obtained were regulated concordantly between the two control clones and the two NKX3.1-expressing clones. The cDNAs that were discordant between the two control clones or between the two NKX3.1-expressing clones were eliminated from the analysis, and the concordant clone expression levels were averaged across the PC-3 control cells and the PC-3(NKX3.1) cells. Then the two mean expression levels were compared. Using a cutoff of 1.4-fold up-regulation or down-regulation, 984 transcripts were identified (Supplementary Table S2). Two separate *IGFBP-3* probes were activated 9.22- and 10.23-fold in PC-3 cells expressing NKX3.1 compared with PC-3 control transfectants. The *IGFBP-3* message differences between control and NKX3.1-expressing cells were the sixth and ninth highest increases of the 508 up-regulated transcripts.

Effect of NKX3.1 on IGFBP-3 expression *in vitro*. To validate the effect of NKX3.1 on IGFBP-3 expression and determine whether protein expression was also affected, we performed Western blotting on a PC-3 clone expressing NKX3.1. NKX3.1 expression was clearly seen in transfected cells, and IGFBP-3 expression was ~10-fold activated compared with control transfected cells (Fig. 1*A*). In a separate transfection experiment, additional PC-3 clones expressing NKX3.1 were isolated. A marked increase was observed for clone 1 in Fig. 1*A*; similar but smaller increases were observed in protein and mRNA in two other clones (Fig. 1*B*).

To show that the apparent induction of IGFBP-3 expression by NKX3.1 was not an adaptation of the cells during clonal selection, we performed Western blotting on PC-3 cells transiently transfected with NKX3.1 and again observed increase expression of IGFBP-3 (Fig. 1*C*). The relationship between expression of NKX3.1 and expression of IGFBP-3 was not exclusive to PC-3 cells because increasing NKX3.1 expression in LNCaP cells by transfection of an NKX3.1 expression vector also increased expression of IGFBP-3 (Fig. 1*C*). Note that exposure to the synthetic androgen R1881 activated NKX3.1 expression but not IGFBP-3. This may be due to proliferative signals of R1881 that interfere with the activation of IGFBP-3 by NKX3.1. Alternatively, LNCaP cells may have down-regulated expression of IGFBP-3 as an adaptation to growth with continuous expression of NKX3.1. However, it should be noted that differences in the medium in which PC-3 and LNCaP cells were cultured may have also contributed to the differences in IGFBP-3 expression in these two cell lines. We also noted that a single probe for *IGFBP-4* was activated 4-fold by NKX3.1 in the expression array analysis. However, increased expression of *IGFBP-4* mRNA was not seen in multiple other PC-3 clones engineered to express NKX3.1 (Fig. 1*D*). LNCaP cells have been shown not to express IGFBP-4 and are used as a negative control in this Western blot, whereas PC-3 cells have been shown to express IGFBP-4 (22). No other IGF binding protein mRNAs were found to be activated in the expression array.

Expression of IGFBP-3 in prostate tissues correlates with expression of NKX3.1. To determine whether the correlation of NKX3.1 and IGFBP-3 expression could also be observed *in vivo*, we analyzed prostate mRNA in *Nkx3.1* gene-targeted mice. We have published quantitation of Nkx3.1 protein in intact, $Nkx3.1^{+/-}$, and $Nkx3.1^{-/-}$ mice, showing that levels of Nkx3.1 protein correlated with gene copy number in Nkx3.1-targeted mice (3). We performed real-time RT-PCR of RNA extracted from these mice. Data in Fig. 2 show that *Igfbp-3* mRNA expression was related to *Nkx3.1* gene copy number in murine prostates. In each reaction, *Gapdh* was used as a control and was invariant between the different strains. We found that in murine prostates, *Igfbp-3* expression levels correlated with *Nkx3.1* copy number and thus with *Nkx3.1* expression (Fig. 2).

Although we had shown an increase in *IGFBP-3* mRNA as a result of NKX3.1 expression in cultured human cells, we were unable to show an effect of NKX3.1 on luciferase reporter constructs that contained regions from the *IGFBP-3* gene promoter (data not shown; ref. 23). This is not entirely surprising because NKX3.1 by itself does not contribute to the formation of a transcriptional complex and suppresses transcription from reporter constructs engineered with the NKX3.1 cognate DNA binding domain (19).

[3] Our unpublished data.

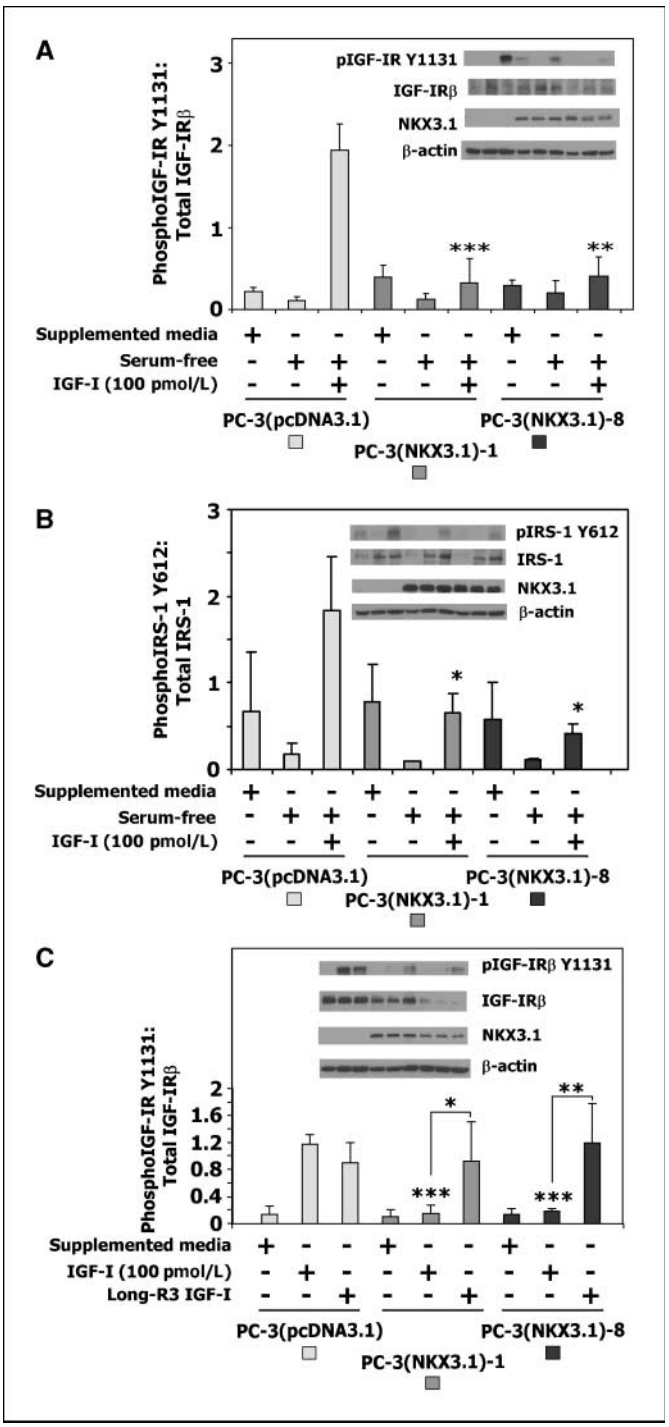

Figure 3. NKX3.1 expression inhibits the IGF-1–mediated phosphorylation of the IGF-1R and IRS-1 in PC-3 cells. *A,* Western blot analysis of extracts from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, and PC-3(NKX3.1)-8 stable cell clones serum starved for 16 h and treated with 100 pmol/L IGF-I. The histogram of IGF-IR activation is based on three separate experiments. *B,* Western blot analysis of extracts from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, and PC-3(NKX3.1)-8 clones serum starved for 16 h and treated with 100 pmol/L IGF-I. The histogram of IRS-1 activation is based on three separate experiments. *C,* Western blot analysis of extracts from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, and PC-3(NKX3.1)-8 clones serum starved for 16 h and treated with 100 pmol/L IGF-1 or long-R3-IGF-I. The histogram of IGF-IR activation is based on three separate experiments. Statistical comparisons are indicated by asterisks as explained in Materials and Methods. Comparisons are versus PC-3(pcDNA3.1) treated with IGF-I unless otherwise indicated by brackets.

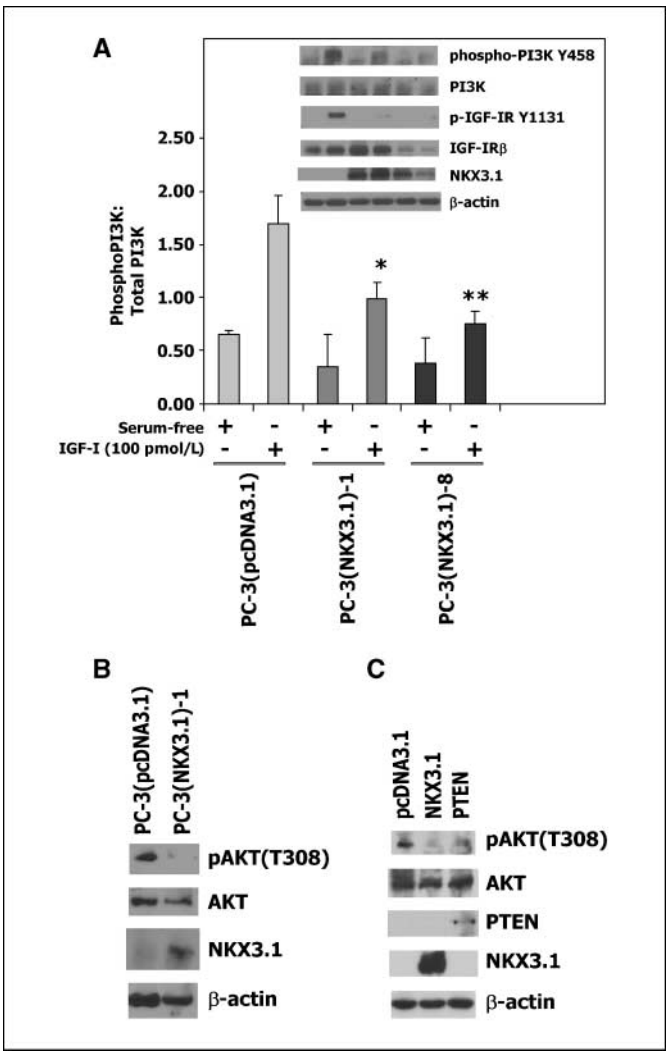

Figure 4. NKX3.1 attenuates IGF-1R downstream signaling. *A,* Western blot analysis of extracts from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, and PC-3(NKX3.1)-8 clones serum starved for 16 h and treated with 100 pmol/L IGF-I for 3 min. The histogram of PI-3K activation is based on three separate experiments. Statistical comparisons are indicated by asterisks. Comparisons are versus PC-3(pcDNA3.1) treated with IGF-I. *B,* Western blot analysis of cell extracts from PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells grown in medium containing 10% FBS. *C,* Western blot analysis of cell extracts of PC-3 cells transiently transfected with either a NKX3.1 or a PTEN expression vector.

The effect of NKX3.1 on IGF-I signaling. To determine whether the induction of IGFBP-3 expression by NKX3.1 affected IGF-I signaling, we examined the response of the IGF-IR to IGF-I in derivative PC-3 cells. In the presence of serum-free medium, IGF-I induced IGF-IR phosphorylation at Tyr^{1131} within 3 minutes of exposure to the ligand (24). Phosphorylation of IGF-IR was diminished in cells expressing NKX3.1 (Fig. 3*A*). The effect of NKX3.1 on IGF-IR activation could also be seen on downstream signaling targets. IGF-I–induced phosphorylation of IRS-1, a target of both the insulin receptor and IGF-IR, was diminished in cells expressing NKX3.1 (Fig. 3*B*). PC-3 derivative cells were also treated with the long-R3-IGF-I that has minimal binding to IGFBP-3 (25, 26). Long-R3-IGF-I activated phosphorylation of IGF-IR equally well in derivative PC-3 cells regardless of NKX3.1 expression (Fig. 3*C*). This result is consistent with the notion that NKX3.1 mediates inhibition of IGF-I signaling via increased expression of IGFBP-3.

We examined the effect of NKX3.1 expression on the phosphorylation of PI3K and its downstream target AKT. PI3K phosphorylation was diminished to some degree by expression of NKX3.1 in two PC-3(NKX3.1) clones (Fig. 4*A*). AKT phosphorylation was also decreased in a PC-3(NKX3.1) clone grown in serum-supplemented medium that contains IGF-I from FBS (Fig. 4*B*). We compared the effects of NKX3.1 expression and PTEN expression in transient transfection of PC-3 cells and saw comparable degrees of reduction in p-AKT (Fig. 4*C*).

Growth suppression by NKX3.1 is mediated by IGFBP-3. *In vitro* growth of the parental and derivative PC-3 cells was assessed by cell counting over 96 hours. As shown in the top section of Table 1, NKX3.1 expression decreased cell proliferation in three independent clones. The doubling times for PC-3 cells expressing NKX3.1 ranged from 25% to 60% above the doubling times for control cells. To determine whether this effect of NKX3.1 expression on cell proliferation was due to IGFBP-3 expression, we performed growth experiments in the presence of a siRNA oligonucleotide and control oligonucleotides for IGFBP-3 knockdown (21). *IGFBP-3* siRNA treatment decreased IGFBP-3 expression at both 24 and 96 hours after cells were exposed to the oligonucleotide (Fig. 5*A*). Growth curves of control and NKX3.1-expressing PC-3 cells were done in the presence of transfection reagent, missense oligonucleotide, and *IGFBP-3* siRNA. Only the *IGFBP-3* siRNA restored PC-3 proliferative rate to the level of the controls (Table 1, *bottom section*). Thus, IGFBP-3 mediates, at least in part, *in vitro* growth suppression by NKX3.1. Consistent with this finding, the IGFBP-3 siRNA reversed the suppression of IGF-IR phosphorylation induced by NKX3.1 (Fig. 5*B*). IGFBP-3 knockdown was accomplished with a single IGFBP-3 siRNA oligonucleotide as described in Materials and Methods. Of the 11 sequences tested, only one induced substantial IGFBP-3 knockdown. This one effective siRNA sequence has no identifiable homology with sequences in other genes, as confirmed by a BLAST search against the entire human genome sequence.

We also performed xenograft experiments wherein PC-3(NKX3.1) clones 1, 2, and 8 and PC-3(cDNA3.1) cells were inoculated into female *NCr/nu* mice. In every instance, we observed tumor growth of derivative PC-3 cells (Supplementary Fig. S1). Each tumor type had lost expression *in vivo* of the NKX3.1 transgene as shown by immunohistochemical analysis. Thus, there was a selection in xenografts for loss of NKX3.1 expression, preventing us from observing any growth-suppressive effects of NKX3.1 on PC-3 cells *in vivo*.

Discussion

NKX3.1 is important for prostate epithelial cell development, growth control, and differentiation (6, 27). Murine *Nkx3.1* is haploinsufficient and loss of a single allele manifests a phenotype similar to homozygous deletion, but with longer latency (6). In early human prostate cancer, we have found that NKX3.1 expression is down-regulated over a broad range, suggesting a complex effect on the development of human prostate cancer (3). It is important to define the pathways of tumorigenesis that are affected by NKX3.1. We argue here that expression of IGFBP-3 is downstream of NKX3.1 and speculate that IGFBP-3 regulates IGF-I action in prostate epithelial cells.

IGFs are peptide growth factors that bind to the IGF-IR to regulate cell growth, differentiation, and apoptosis (12). IGFs are present in abundance in the circulation and may exert systemic and local effects on cells. Circulating IGF-I is bound mainly to IGFBP-3, one of the most abundant serum proteins (28). Although IGFBP-3 can inhibit the interaction of IGF-I with its receptor at the cellular level, serum IGFBP-3 serves to stabilize circulating IGF-I (29). Serum levels of both proteins vary with age, nutrition, and hormonal status (30). The interaction of serum IGF-I and IGFBP-3 and prostate cancer risk has been studied by a number of investigators (29). The majority of studies have found an association between higher IGF-I levels and prostate cancer

Table 1. Effect of IGFBP-3 knockdown on cell proliferation

Cell line	Treatment	Doubling time (h)	*P*
PC-3	None	25.34 ± 1.91	NS
PC-3(pcDNA3.1)	None	24.26 ± 2.05	Reference
PC-3(NKX3.1)-1	None	32.24 ± 5.91	0.0037
PC-3(NKX3.1)-2a	None	38.88 ± 7.82	0.0002
PC-3(NKX3.1)-8	None	30.24 ± 2.55	0.002
PC-3(pcDNA3.1)	None	23.6 ± 2.52	Reference
PC-3(pcDNA3.1)	Mock	25.5 ± 1.23	NS
PC-3(pcDNA3.1)	Missense oligo	24.4 ± 1.86	NS
PC-3(pcDNA3.1)	IGFBP-3 siRNA oligo	26.4 ± 1.40	NS
PC-3(NKX3.1)-1	None	32.9 ± 1.33	0.0092
PC-3(NKX3.1)-1	Mock	31.7 ± 2.49	0.0013
PC-3(NKX3.1)-1	Missense oligo	32.0 ± 3.12	0.0022
PC-3(NKX3.1)-1	IGFBP-3 siRNA oligo	24.9 ± 2.56	NS

NOTE: The cell doubling time, in hours, of parental PC-3 cells, PC-3(pcDNA3.1) cells, and PC-3(NKX3.1) clones was assayed by cell counting. Cells were counted at 24, 48, 72, and 96 h after seeding and doubling times were calculated. In the bottom section of the table, PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells were treated with transfection reagent alone, the missense siRNA oligonucleotide, and the IGFBP-3 siRNA oligonucleotide for 24 h before the first cell count was taken. *P* values were calculated in comparison with the PC-3(pcDNA3.1) cell doubling time, using ANOVA.
Abbreviation: NS, not significant ($P > 0.05$).

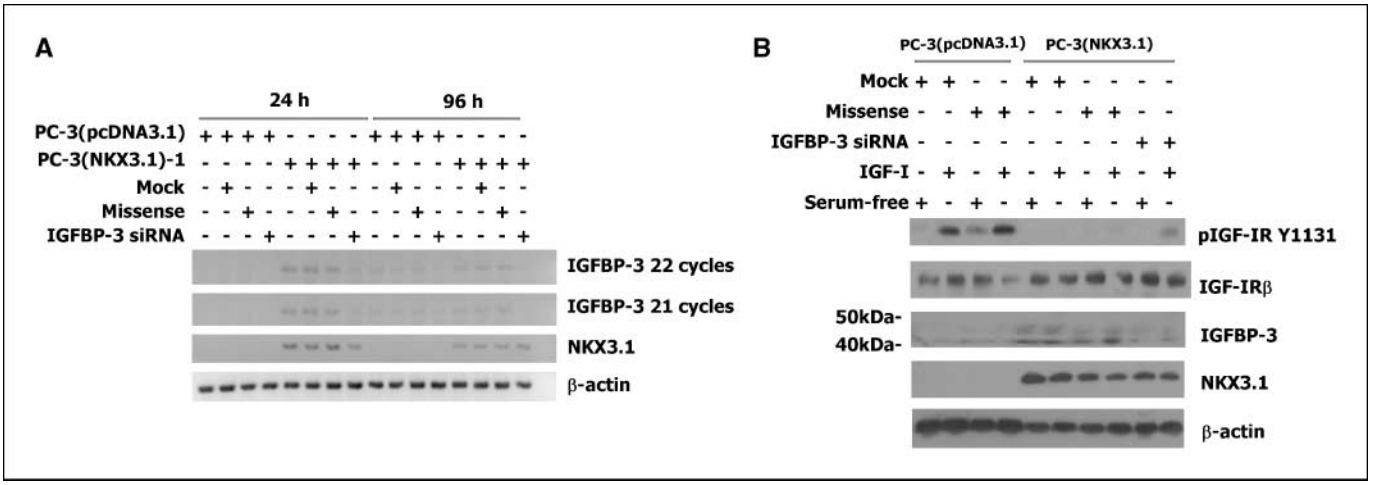

Figure 5. IGFBP-3 knockdown in PC-3(NKX3.1) cells. *A,* RT-PCR analysis of mRNA from PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells that were treated with transfection reagent alone, missense oligo, or the IGFBP-3 siRNA oligo at 24 and 96 h posttransfection. *B,* Western blot analysis of extracts from PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells treated with transfection reagent alone, missense oligo, or the IGFBP-3 siRNA oligo for 96 h, which afterward were serum starved for 16 h and treated with 100 pmol/L IGF-I.

(31–39). Some investigators have not been able to confirm these findings (40–42).

NKX3.1 haploinsufficiency affects cell transformation, at least in part, by downstream effects on transcriptional targets. NKX3.1 binds to DNA and suppresses expression of genes downstream from cognate DNA binding sites (19). We have yet to identify a promoter that is transcriptionally activated by direct binding of NXK3.1 to its cognate DNA -TAAGTA- sequence. In fact, our experiments with reporter constructs containing NKX3.1 binding DNA suggested that NKX3.1 alone cannot initiate assembly of a transcriptional complex (19). NKX3.1 is known to interact with other transcription factors such as serum response factor and serves as a synergistic coactivator of promoters with serum response elements such as smooth muscle γ-actin (43). Therefore, the effect of NKX3.1 on gene expression is complex and is likely mediated by a number of cofactors. Because other NK homeodomain protein family members like Nkx2.5 interact with serum response factor, the physical interaction of NKX3.1 and serum response factor has been studied as a model for transcription factor interactions of NKX3.1. Serum response factor is a widely expressed transcription factor involved in orchestrating disparate programs of gene expression linked to muscle differentiation and cellular growth (44). It is likely that different targets of transcriptional activation are affected by the interaction of NKX3.1 with several different transcription factors.

We have shown an indirect link between NKX3.1 and transcription of IGFBP-3 mRNA. In cultured cells with NKX3.1 overexpression, we have shown a mechanistic link between NKX3.1, IGFBP-3 expression, IGF-IR activation, and cell proliferation. IGF1-R signaling is complex and affected by many factors that regulate IGF-I availability and intracellular signaling downstream from the IGF-IR. Therefore, the interaction between NKX3.1 and IGFBP-3 expression *in vivo* is likely to be part of a more complex system regulating the effect of IGF-I on prostate epithelial cells. The IGFBPs have functions that can compensate for one another, making it difficult to determine specific functions of a single IGF binding protein by studies of gene-targeted mice (45, 46). Whether the same compensatory activation of IGF binding proteins occurs in prostate epithelial cells that have reduced NKX3.1 expression was not determined.

Down-regulation of NKX3.1 protein per se is sufficient to predispose cells to malignant transformation. In addition, we have described a family in which hereditary prostate cancer cosegregated with a T164A missense mutation in the NKX3.1 homeodomain that reduced DNA binding by 95% (47). Haploinsufficiency is a reflection of the dominant nature of regulation by NK family members. Both missense and truncation mutations in NKX2.5 are autosomal dominant determinants of congenital cardiac abnormalities (48, 49). Similarly, mutations in NKX2.1/TTF cause pulmonary and thyroid developmental abnormalities (50). Paradoxically, *NKX2.1* is amplified in a subset of lung cancers and NKX2.1 overexpression contributes to cell transformation and oncogenesis (51). We argue that tumor suppression by NKX3.1 is exerted in a relative manner by modulation of downstream targets to different degrees. Our finding that IGFBP-3 expression in human prostate cancer cells correlates quantitatively with NKX3.1 expression levels is reminiscent of findings that *Nkx3.1* gene dosage determines the degree of transcriptional effects in gene-targeted mice (8). Further studies will identify additional NKX3.1 targets and elucidate their role in prostate cancer suppression and, perhaps, prevention.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

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Supplementary Table 1
siRNA Oligonucleotide Sequences not Used for IGFBP-3 Knockdown

siRNA Sequence	**nucleotides**	**Source**
GCUACAAAGUUGACUACGA	686-704	ON-TARGET Plus SMART pool sequences
GAAAUGCUAGUGAGUCGGA	536-554	ON-TARGET Plus SMART pool sequences
GCACAGAUACCCAGAACUU	713-731	ON-TARGET Plus SMART pool sequences
GAAUAUGGUCCCUGCCGUA	757-775	ON-TARGET Plus SMART pool sequences
UAUCGAGAAUAGGAAAACC	1427-1445	siDESIGN center
GCAGCCUCUCCCAGGCUACA	940-958	siDESIGN center
GCAUAAGCUCUUUAAAGGCA	1895-1913	siDESIGN center
UGCCUGGAUUCCACAGCUU	44-62	siDESIGN center
AAGCAGCGTGCCCCGGUUG	106-124	siDESIGN center
AAAGGCAAAGCUUUAUUUU	1908-1926	siDESIGN center

Oligonucleotide sequences used for siRNA oligonucleotides tested to induce *IGFBP-3* knockdown. Sequences 1-4 were from ON-TARGET Plus SMART pool sequences (Cat. # L-004777-00-0005, Dharmacon, Lafayette, CO). Sequences 5-10 were generated in our laboratory using the siDESIGN center from the Dharmacon website (www.dharmacon.com) by inputting the Genbank accession number NM_000598 (IGFBP-3).

Supplementary Table 2

Transcripts Activated by NKX3.1 in PC-3 Cells

PC-3 cells were stably transfected with the pcDNA3.1 empty vector or NKX3.1 expression vector and mRNA from two clones of each cell type was isolated for microarray analysis on the Affymetrix U-133 expression array. Analyses of results from each pair of clones of the same genotype that did not match up were discarded to ensure clonal variation was not a factor. 984 genes were found to be up- or down-regulated more that 1.4 fold in the NKX3.1 expressing PC-3 cells, in comparison to the PC-3 control cells. The 6^{th} and 9^{th} most activated probe sets were for human growth hormone-dependent insulin-like growth factor-binding protein, now known as IGFBP-3.

Supplementary Table 2

NAME	Fold Change	Description
204081_at	17.93	gb:NM_006176.1 /DEF=Homo sapiens neurogranin (protein kinase C substrate, RC3) (NRGN), mRNA. /FEA=mRNA /GEN=NRGN /PROD=neurogranin /DB_XREF=gi:5453799 /UG=Hs.26944 neurogranin (protein kinase C substrate, RC3) /FL=gb:BC002835.1 gb:U89165.1 gb:NM_006176.1
205067_at	14.79	gb:NM_000576.1 /DEF=Homo sapiens interleukin 1, beta (IL1B), mRNA. /FEA=mRNA /GEN=IL1B /PROD=interleukin 1, beta /DB_XREF=gi:10835144 /UG=Hs.126256 interleukin 1, beta /FL=gb:NM_000576.1 gb:K02770.1 gb:M15330.1 gb:M54933.1
39402_at	11.88	Cluster Incl. M15330:Human interleukin 1-beta (IL1B) mRNA, complete cds /cds=(86,895) /gb=M15330 /gi=186283 /ug=Hs.126256 /len=1497
204953_at	11.53	gb:NM_014841.1 /DEF=Homo sapiens KIAA0656 gene product (KIAA0656), mRNA. /FEA=mRNA /GEN=KIAA0656 /PROD=KIAA0656 gene product /DB_XREF=gi:7662227 /UG=Hs.12477 synaptosomal-associated protein, 91 kDa (mouse) homolog /FL=gb:AB014556.1 gb:NM_014841.1
209372_x_at	10.61	Consensus includes gb:BF971587 /FEA=EST /DB_XREF=gi:12338802 /DB_XREF=est:602239834F1 /CLONE=IMAGE:4328385 /UG=Hs.179661 tubulin, beta polypeptide /FL=gb:BC001352.1
210095_s_at	10.23	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, complete cds. /FEA=mRNA /GEN=IGFBP1 /DB_XREF=gi:183115 /UG=Hs.77326 insulin-like growth factor binding protein 3 /FL=gb:BC000013.1 gb:M31159.1
207714_s_at	9.61	gb:NM_004353.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 (SERPINH1), mRNA. /FEA=mRNA /GEN=SERPINH1 /PROD=serine (or cysteine) proteinase inhibitor, cladeH (heat shock protein 47), member 1 /DB_XREF=gi:4757923 /UG=Hs.241579 serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 /FL=gb:NM_004353.1
208581_x_at	9.26	gb:NM_005952.1 /DEF=Homo sapiens metallothionein 1X (MT1X), mRNA. /FEA=CDS /GEN=MT1X /PROD=metallothionein 1X /DB_XREF=gi:10835231 /UG=Hs.278462 metallothionein 1X /FL=gb:NM_005952.1
212143_s_at	9.22	Consensus includes gb:BF340228 /FEA=EST /DB_XREF=gi:11286690 /DB_XREF=est:602036816F1 /CLONE=IMAGE:4185050 /UG=Hs.77326 insulin-like growth factor binding protein 3 /FL=gb:NM_000598.1
204614_at	9.18	gb:NM_002575.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA. /FEA=mRNA /GEN=SERPINB2 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 2 /DB_XREF=gi:4505594 /UG=Hs.75716 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 /FL=gb:J02685.1 gb:J03603.1 gb:M18082.1 gb:NM_002575.1
209118_s_at	8.33	gb:AF141347.1 /DEF=Homo sapiens hum-a-tub2 alpha-tubulin mRNA, complete cds. /FEA=mRNA /PROD=alpha-tubulin /DB_XREF=gi:4929133 /UG=Hs.272897 Tubulin, alpha, brain-specific /FL=gb:AF141347.1 gb:NM_006009.1
216971_s_at	7.97	Consensus includes gb:Z54367 /DEF=H.sapiens gene for plectin /FEA=CDS /DB_XREF=gi:1296661 /UG=Hs.79706 plectin 1, intermediate filament binding protein, 500kD
204247_s_at	7.83	gb:NM_004935.1 /DEF=Homo sapiens cyclin-dependent kinase 5 (CDK5), mRNA. /FEA=mRNA /GEN=CDK5 /PROD=cyclin-dependent kinase 5 /DB_XREF=gi:4826674 /UG=Hs.166071 cyclin-dependent kinase 5 /FL=gb:BC005115.1 gb:NM_004935.1
203921_at	7.48	gb:NM_004267.1 /DEF=Homo sapiens carbohydrate (chondroitin 6keratan) sulfotransferase 2 (CHST2), mRNA. /FEA=mRNA /GEN=CHST2 /PROD=carbohydrate (chondroitin 6keratan)sulfotransferase 2 /DB_XREF=gi:4757983 /UG=Hs.8786 carbohydrate (chondroitin 6keratan) sulfotransferase 2 /FL=gb:AB021124.1 gb:AB014679.1 gb:AB014680.1 gb:AF083066.1 gb:NM_004267.1

204222_s_at	7.24	gb:NM_006851.1 /DEF=Homo sapiens glioma pathogenesis-related protein (RTVP1), mRNA. /FEA=mRNA /GEN=RTVP1 /PROD=glioma pathogenesis-related protein /DB_XREF=gi:5803150 /UG=Hs.64639 glioma pathogenesis-related protein /FL=gb:U16307.1 gb:NM_006851.1
209215_at	7.24	gb:L11669.1 /DEF=Human tetracycline transporter-like protein mRNA, complete cds. /FEA=mRNA /PROD=tetracycline transporter-like protein /DB_XREF=gi:307501 /UG=Hs.157145 tetracycline transporter-like protein /FL=gb:L11669.1 gb:NM_001120.1
219140_s_at	7.18	gb:NM_006744.2 /DEF=Homo sapiens retinol-binding protein 4, interstitial (RBP4), mRNA. /FEA=mRNA /GEN=RBP4 /PROD=retinol-binding protein 4, interstitialprecursor /DB_XREF=gi:8400727 /UG=Hs.76461 retinol-binding protein 4, interstitial /FL=gb:AF119868.1 gb:NM_006744.2
222242_s_at	7.13	Consensus includes gb:AF243527 /DEF=Homo sapiens serine protease gene cluster, complete sequence /FEA=CDS_12 /DB_XREF=gi:11244757 /UG=Hs.50915 kallikrein 5
211456_x_at	6.98	gb:AF333388.1 /DEF=Homo sapiens metallothionein 1H-like protein mRNA, complete cds. /FEA=mRNA /PROD=metallothionein 1H-like protein /DB_XREF=gi:13310411 /UG=Hs.326774 Homo sapiens metallothionein 1H-like protein mRNA, complete cds /FL=gb:AF333388.1
219922_s_at	6.91	gb:NM_021070.1 /DEF=Homo sapiens latent transforming growth factor beta binding protein 3 (LTBP3), mRNA. /FEA=mRNA /GEN=LTBP3 /PROD=latent transforming growth factor beta bindingprotein 3 /DB_XREF=gi:10835104 /UG=Hs.289019 latent transforming growth factor beta binding protein 3 /FL=gb:NM_021070.1 gb:AF135960.2
201739_at	6.84	gb:NM_005627.1 /DEF=Homo sapiens serumglucocorticoid regulated kinase (SGK), mRNA. /FEA=mRNA /GEN=SGK /PROD=serumglucocorticoid regulated kinase /DB_XREF=gi:5032090 /UG=Hs.296323 serumglucocorticoid regulated kinase /FL=gb:BC001263.1 gb:NM_005627.1 gb:AF153609.1
206026_s_at	6.74	gb:NM_007115.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA. /FEA=mRNA /GEN=TNFAIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /DB_XREF=gi:6005905 /UG=Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM_007115.1
221972_s_at	6.72	Consensus includes gb:AL571362 /FEA=EST /DB_XREF=gi:12928582 /DB_XREF=est:AL571362 /CLONE=CS0DI009YD14 (3 prime) /UG=Hs.42806 calcium binding protein Cab45 precursor,
204115_at	6.52	gb:NM_004126.1 /DEF=Homo sapiens guanine nucleotide binding protein 11 (GNG11), mRNA. /FEA=mRNA /GEN=GNG11 /PROD=guanine nucleotide binding protein 11 /DB_XREF=gi:4758447 /UG=Hs.83381 guanine nucleotide binding protein 11 /FL=gb:NM_004126.1 gb:U31384.1
213887_s_at	6.27	Consensus includes gb:AI554759 /FEA=EST /DB_XREF=gi:4487122 /DB_XREF=est:tn30e02.x1 /CLONE=IMAGE:2169146 /UG=Hs.24301 polymerase (RNA) II (DNA directed) polypeptide E (25kD)
215617_at	6.11	Consensus includes gb:AU145711 /FEA=EST /DB_XREF=gi:11007232 /DB_XREF=est:AU145711 /CLONE=HEMBA1005588 /UG=Hs.301006 Homo sapiens cDNA FLJ11754 fis, clone HEMBA1005588
221521_s_at	6.03	gb:BC003186.1 /DEF=Homo sapiens, HSPC037 protein, clone MGC:673, mRNA, complete cds. /FEA=mRNA /PROD=HSPC037 protein /DB_XREF=gi:13112024 /UG=Hs.108196 HSPC037 protein /FL=gb:BC003186.1 gb:AF201939.1
210792_x_at	5.96	gb:AF033111.1 /DEF=Homo sapiens Siva-2 mRNA, complete cds. /FEA=mRNA /PROD=Siva-2 /DB_XREF=gi:5737690 /UG=Hs.112058 CD27-binding (Siva) protein /FL=gb:NM_021709.1 gb:AF033111.1
216080_s_at	5.79	Consensus includes gb:AC004770 /DEF=Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene /FEA=CDS_3 /DB_XREF=gi:3212836 /UG=Hs.21765 fatty acid desaturase 3
204733_at	5.74	gb:NM_002774.1 /DEF=Homo sapiens kallikrein 6 (neurosin, zyme) (KLK6), mRNA. /FEA=mRNA /GEN=KLK6 /PROD=kallikrein 6 (neurosin, zyme) /DB_XREF=gi:4506154 /UG=Hs.79361 kallikrein 6 (neurosin, zyme) /FL=gb:U62801.1 gb:D78203.1 gb:AF013988.1 gb:NM_002774.1

209278_s_at	5.65	gb:L27624.1 /DEF=Homo sapiens tissue factor pathway inhibitor-2 mRNA, complete cds. /FEA=mRNA /PROD=tissue factor pathway inhibitor-2 /DB_XREF=gi:441149 /UG=Hs.295944 tissue factor pathway inhibitor 2 /FL=gb:BC005330.1 gb:L27624.1 gb:D29992.1 gb:NM_006528.1
204326_x_at	5.64	gb:NM_002450.1 /DEF=Homo sapiens metallothionein 1L (MT1L), mRNA. /FEA=mRNA /GEN=MT1L /PROD=metallothionein 1L /DB_XREF=gi:4505270 /UG=Hs.94360 metallothionein 1L /FL=gb:NM_002450.1
215646_s_at	5.54	Consensus includes gb:R94644 /FEA=EST /DB_XREF=gi:970039 /DB_XREF=est:yq42a12.r1 /CLONE=IMAGE:198430 /UG=Hs.306542 Homo sapiens versican Vint isoform, mRNA, partial cds
217165_x_at	5.5	Consensus includes gb:M10943 /DEF=Human metallothionein-If gene (hMT-If) /FEA=CDS /DB_XREF=gi:187540 /UG=Hs.203936 metallothionein 1F (functional)
204748_at	5.49	gb:NM_000963.1 /DEF=Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) (PTGS2), mRNA. /FEA=mRNA /GEN=PTGS2 /PROD=prostaglandin-endoperoxide synthase 2(prostaglandin GH synthase and cyclooxygenase) /DB_XREF=gi:4506264 /UG=Hs.196384 prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase) /FL=gb:M90100.1 gb:L15326.1 gb:NM_000963.1
221731_x_at	5.48	Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:11112418 /DB_XREF=est:601885091F1 /CLONE=IMAGE:4103447 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican)
204932_at	5.45	Consensus includes gb:BF433902 /FEA=EST /DB_XREF=gi:11446030 /DB_XREF=est:7q56c10.x1 /CLONE=IMAGE:3702163 /UG=Hs.81791 tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) /FL=gb:U94332.1 gb:AB002146.1 gb:NM_002546.1
212764_at	5.43	Consensus includes gb:AI806174 /FEA=EST /DB_XREF=gi:5392740 /DB_XREF=est:wf06h03.x1 /CLONE=IMAGE:2349845 /UG=Hs.232068 transcription factor 8 (represses interleukin 2 expression)
208960_s_at	5.42	Consensus includes gb:BE675435 /FEA=EST /DB_XREF=gi:10035976 /DB_XREF=est:7f09a11.x1 /CLONE=IMAGE:3294140 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM_001300.2
212185_x_at	5.26	Consensus includes gb:NM_005953.1 /DEF=Homo sapiens metallothionein 2A (MT2A), mRNA. /FEA=CDS /GEN=MT2A /PROD=metallothionein 2A /DB_XREF=gi:5174763 /UG=Hs.118786 metallothionein 2A /FL=gb:NM_005953.1
204620_s_at	5.26	gb:NM_004385.1 /DEF=Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA. /FEA=mRNA /GEN=CSPG2 /PROD=chondroitin sulfate proteoglycan 2 (versican) /DB_XREF=gi:4758081 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican) /FL=gb:NM_004385.1
218585_s_at	5.12	gb:NM_016448.1 /DEF=Homo sapiens L2DTL protein (L2DTL), mRNA. /FEA=mRNA /GEN=L2DTL /PROD=L2DTL protein /DB_XREF=gi:7705575 /UG=Hs.126774 L2DTL protein /FL=gb:AF195765.1 gb:NM_016448.1
202855_s_at	5	Consensus includes gb:AL513917 /FEA=EST /DB_XREF=gi:12777411 /DB_XREF=est:AL513917 /CLONE=CL0BA006ZD09 (3 prime) /UG=Hs.85838 solute carrier family 16 (monocarboxylic acid transporters), member 3 /FL=gb:U81800.1 gb:NM_004207.1
204584_at	4.99	Consensus includes gb:AI653981 /FEA=EST /DB_XREF=gi:4737960 /DB_XREF=est:ty04c03.x1 /CLONE=IMAGE:2278084 /UG=Hs.1757 L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1) /FL=gb:NM_024003.1 gb:NM_000425.2 gb:M77640.1 gb:M74387.1
204775_at	4.98	gb:NM_005441.1 /DEF=Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA. /FEA=mRNA /GEN=CHAF1B /PROD=chromatin assembly factor 1, subunit B (p60) /DB_XREF=gi:4885104 /UG=Hs.75238 chromatin assembly factor 1, subunit B (p60) /FL=gb:NM_005441.1 gb:U20980.1
202779_s_at	4.95	gb:NM_014501.1 /DEF=Homo sapiens ubiquitin carrier protein (E2-EPF), mRNA. /FEA=mRNA /GEN=E2-EPF

		/PROD=ubiquitin carrier protein /DB_XREF=gi:7657045 /UG=Hs.174070 ubiquitin carrier protein /FL=gb:M91670.1 gb:NM_014501.1
206461_x_at	4.84	gb:NM_005951.1 /DEF=Homo sapiens metallothionein 1H (MT1H), mRNA. /FEA=mRNA /GEN=MT1H /PROD=metallothionein 1H /DB_XREF=gi:10835084 /UG=Hs.2667 metallothionein 1H /FL=gb:NM_005951.1
204338_s_at	4.8	gb:NM_005613.2 /DEF=Homo sapiens regulator of G-protein signalling 4 (RGS4), mRNA. /FEA=mRNA /GEN=RGS4 /PROD=regulator of G-protein signaling 4 /DB_XREF=gi:11184227 /UG=Hs.227571 regulator of G-protein signalling 4 /FL=gb:NM_005613.2 gb:BC000737.1
222155_s_at	4.77	Consensus includes gb:AK021918.1 /DEF=Homo sapiens cDNA FLJ11856 fis, clone HEMBA1006789. /FEA=mRNA /DB_XREF=gi:10433214 /UG=Hs.6459 hypothetical protein FLJ11856
214974_x_at	4.75	Consensus includes gb:AK026546.1 /DEF=Homo sapiens cDNA: FLJ22893 fis, clone KAT04792. /FEA=mRNA /DB_XREF=gi:10439427 /UG=Hs.287716 Homo sapiens cDNA: FLJ22893 fis, clone KAT04792
219691_at	4.74	gb:NM_017654.1 /DEF=Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA. /FEA=mRNA /GEN=FLJ20073 /PROD=hypothetical protein FLJ20073 /DB_XREF=gi:8923080 /UG=Hs.65641 hypothetical protein FLJ20073 /FL=gb:NM_017654.1
202326_at	4.69	gb:NM_006709.1 /DEF=Homo sapiens ankyrin repeat-containing protein (G9A), mRNA. /FEA=mRNA /GEN=G9A /PROD=ankyrin repeat-containing protein /DB_XREF=gi:5729833 /UG=Hs.75196 ankyrin repeat-containing protein /FL=gb:BC002686.1 gb:NM_006709.1
204306_s_at	4.68	gb:NM_004357.1 /DEF=Homo sapiens CD151 antigen (CD151), mRNA. /FEA=mRNA /GEN=CD151 /PROD=CD151 antigen /DB_XREF=gi:4757941 /UG=Hs.75564 CD151 antigen /FL=gb:BC001374.1 gb:D29963.1 gb:NM_004357.1 gb:U14650.1
219491_at	4.57	gb:NM_024036.1 /DEF=Homo sapiens hypothetical protein MGC3103 (MGC3103), mRNA. /FEA=mRNA /GEN=MGC3103 /PROD=hypothetical protein MGC3103 /DB_XREF=gi:13128987 /UG=Hs.115960 hypothetical protein MGC3103 /FL=gb:BC000207.1 gb:NM_024036.1
208394_x_at	4.56	gb:NM_007036.2 /DEF=Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA. /FEA=mRNA /GEN=ESM1 /PROD=endothelial cell-specific molecule 1 precursor /DB_XREF=gi:13259505 /UG=Hs.41716 endothelial cell-specific molecule 1 /FL=gb:NM_007036.2
214240_at	4.52	Consensus includes gb:AL556409 /FEA=EST /DB_XREF=gi:12899058 /DB_XREF=est:AL556409 /CLONE=CS0DK004YA08 (5 prime) /UG=Hs.1907 galanin
212242_at	4.5	Consensus includes gb:AL565074 /FEA=EST /DB_XREF=gi:12916087 /DB_XREF=est:AL565074 /CLONE=CS0DN003YF20 (3 prime) /UG=Hs.75318 tubulin, alpha 1 (testis specific)
204441_s_at	4.5	gb:NM_002689.1 /DEF=Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA. /FEA=mRNA /GEN=POLA2 /PROD=polymerase (DNA-directed), alpha (70kD) /DB_XREF=gi:4505928 /UG=Hs.81942 polymerase (DNA-directed), alpha (70kD) /FL=gb:BC001347.1 gb:BC002990.1 gb:L24559.1 gb:NM_002689.1
201373_at	4.5	gb:NM_000445.1 /DEF=Homo sapiens plectin 1, intermediate filament binding protein, 500kD (PLEC1), mRNA. /FEA=mRNA /GEN=PLEC1 /PROD=plectin 1, intermediate filament bindingprotein, 500kD /DB_XREF=gi:4505876 /UG=Hs.79706 plectin 1, intermediate filament binding protein, 500kD /FL=gb:U53204.1 gb:NM_000445.1
204597_x_at	4.46	gb:NM_003155.1 /DEF=Homo sapiens stanniocalcin 1 (STC1), mRNA. /FEA=mRNA /GEN=STC1 /PROD=stanniocalcin 1 /DB_XREF=gi:4507264 /UG=Hs.25590 stanniocalcin 1 /FL=gb:U46768.1 gb:U25997.1 gb:NM_003155.1
203680_at	4.42	gb:NM_002736.1 /DEF=Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA. /FEA=mRNA /GEN=PRKAR2B /PROD=protein kinase, cAMP-dependent, regulatory, typeII, beta /DB_XREF=gi:4506064 /UG=Hs.77439 protein kinase, cAMP-dependent, regulatory, type II, beta /FL=gb:M31158.1 gb:NM_002736.1

218332_at	4.41	gb:NM_018476.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HBEX2 (HBEX2), mRNA. /FEA=mRNA /GEN=HBEX2 /PROD=uncharacterized hypothalamus protein HBEX2 /DB_XREF=gi:8923715 /UG=Hs.283719 uncharacterized hypothalamus protein HBEX2 /FL=gb:AF220189.1 gb:NM_018476.1 gb:AF183416.1 gb:AF237783.1
216250_s_at	4.39	Consensus includes gb:X77598.1 /DEF=H.sapiens LAM A3 mRNA for laminin alpha 3 chain. /FEA=mRNA /DB_XREF=gi:9716101 /UG=Hs.83450 laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)
202917_s_at	4.38	gb:NM_002964.2 /DEF=Homo sapiens S100 calcium-binding protein A8 (calgranulin A) (S100A8), mRNA. /FEA=mRNA /GEN=S100A8 /PROD=S100 calcium-binding protein A8 /DB_XREF=gi:9845519 /UG=Hs.100000 S100 calcium-binding protein A8 (calgranulin A) /FL=gb:NM_002964.2
209126_x_at	4.37	gb:L42612.1 /DEF=Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds. /FEA=mRNA /GEN=KRT6F /PROD=keratin type II /DB_XREF=gi:908804 /UG=Hs.111758 keratin 6A /FL=gb:NM_005554.1 gb:L42611.1 gb:L42612.1
217716_s_at	4.35	gb:NM_013336.1 /DEF=Homo sapiens sec61 homolog (HSEC61), mRNA. /FEA=mRNA /GEN=HSEC61 /PROD=sec61 homolog /DB_XREF=gi:7019414 /UG=Hs.306079 sec61 homolog /FL=gb:BC002951.1 gb:AF346602.1 gb:AF084458.1 gb:NM_013336.1
217854_s_at	4.23	gb:NM_002695.1 /DEF=Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E), mRNA. /FEA=mRNA /GEN=POLR2E /PROD=polymerase (RNA) II (DNA directed) polypeptide E(25kD) /DB_XREF=gi:4505944 /UG=Hs.24301 polymerase (RNA) II (DNA directed) polypeptide E (25kD) /FL=gb:BC004441.1 gb:NM_002695.1 gb:J04965.1 gb:D38251.1
212141_at	4.16	Consensus includes gb:AA604621 /FEA=EST /DB_XREF=gi:2445485 /DB_XREF=est:no84b08.s1 /CLONE=IMAGE:1113495 /UG=Hs.154443 minichromosome maintenance deficient (S. cerevisiae) 4
213746_s_at	4.14	Consensus includes gb:AW051856 /FEA=EST /DB_XREF=gi:5914215 /DB_XREF=est:wz04a05.x1 /CLONE=IMAGE:2557040 /UG=Hs.195464 filamin A, alpha (actin-binding protein-280)
208750_s_at	4.14	Consensus includes gb:AA580004 /FEA=EST /DB_XREF=gi:2355331 /DB_XREF=est:nl79c05.s1 /CLONE=IMAGE:1056872 /UG=Hs.74571 ADP-ribosylation factor 1 /FL=gb:M84326.1 gb:M36340.1 gb:AF055002.1 gb:AF052179.1 gb:NM_001658.2
204745_x_at	4.14	gb:NM_005950.1 /DEF=Homo sapiens metallothionein 1G (MT1G), mRNA. /FEA=mRNA /GEN=MT1G /PROD=metallothionein 1G /DB_XREF=gi:10835229 /UG=Hs.173451 metallothionein 1G /FL=gb:NM_005950.1
201508_at	4.12	gb:NM_001552.1 /DEF=Homo sapiens insulin-like growth factor-binding protein 4 (IGFBP4), mRNA. /FEA=mRNA /GEN=IGFBP4 /PROD=insulin-like growth factor-binding protein 4 /DB_XREF=gi:10835020 /UG=Hs.1516 insulin-like growth factor-binding protein 4 /FL=gb:NM_001552.1 gb:M62403.1
213680_at	4.12	Consensus includes gb:AI831452 /FEA=EST /DB_XREF=gi:5452123 /DB_XREF=est:wj49b03.x1 /CLONE=IMAGE:2406125 /UG=Hs.111758 keratin 6A
209589_s_at	4.1	gb:AF025304.1 /DEF=Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA, complete cds. /FEA=mRNA /GEN=EPHB2 /PROD=protein-tyrosine kinase EPHB2v /DB_XREF=gi:2739055 /UG=Hs.125124 EphB2 /FL=gb:AF025304.1
201482_at	4.08	gb:NM_002826.2 /DEF=Homo sapiens quiescin Q6 (QSCN6), mRNA. /FEA=mRNA /GEN=QSCN6 /PROD=quiescin Q6 /DB_XREF=gi:13325074 /UG=Hs.77266 quiescin Q6 /FL=gb:L42379.1 gb:U97276.2 gb:NM_002826.2
202338_at	4.01	gb:NM_003258.1 /DEF=Homo sapiens thymidine kinase 1, soluble (TK1), mRNA. /FEA=mRNA /GEN=TK1 /PROD=thymidine kinase 1, soluble /DB_XREF=gi:4507518 /UG=Hs.105097 thymidine kinase 1, soluble /FL=gb:K02581.1 gb:NM_003258.1
222162_s_at	3.99	Consensus includes gb:AK023795.1 /DEF=Homo sapiens cDNA FLJ13733 fis, clone PLACE3000147, highly

		similar to Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA. /FEA=mRNA /DB_XREF=gi:10435838 /UG=Hs.8230 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1
204070_at	3.91	gb:NM_004585.2 /DEF=Homo sapiens retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA. /FEA=mRNA /GEN=RARRES3 /PROD=retinoic acid receptor responder (tazaroteneinduced) 3 /DB_XREF=gi:8051633 /UG=Hs.17466 retinoic acid receptor responder (tazarotene induced) 3 /FL=gb:AF060228.1 gb:AF092922.1 gb:NM_004585.2 gb:AB030815.1
204595_s_at	3.89	Consensus includes gb:AI300520 /FEA=EST /DB_XREF=gi:3959866 /DB_XREF=est:qn55e06.x1 /CLONE=IMAGE:1902178 /UG=Hs.25590 stanniocalcin 1 /FL=gb:U46768.1 gb:U25997.1 gb:NM_003155.1
32209_at	3.89	Cluster Incl. AF052151:Homo sapiens clone 24574 mRNA sequence /cds=UNKNOWN /gb=AF052151 /gi=3360461 /ug=Hs.18686 /len=1337
202856_s_at	3.88	gb:NM_004207.1 /DEF=Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3), mRNA. /FEA=mRNA /GEN=SLC16A3 /PROD=solute carrier family 16 (monocarboxylic acidtransporters), member 3 /DB_XREF=gi:4759111 /UG=Hs.85838 solute carrier family 16 (monocarboxylic acid transporters), member 3 /FL=gb:U81800.1 gb:NM_004207.1
202154_x_at	3.88	gb:NM_006086.1 /DEF=Homo sapiens tubulin, beta, 4 (TUBB4), mRNA. /FEA=mRNA /GEN=TUBB4 /PROD=tubulin, beta, 4 /DB_XREF=gi:5174736 /UG=Hs.159154 tubulin, beta, 4 /FL=gb:BC000748.1 gb:U47634.1 gb:NM_006086.1
208937_s_at	3.86	gb:D13889.1 /DEF=Human mRNA for Id-1H, complete cds. /FEA=mRNA /GEN=Id-1H /PROD=Id-1H /DB_XREF=gi:464181 /UG=Hs.75424 inhibitor of DNA binding 1, dominant negative helix-loop-helix protein /FL=gb:BC000613.1 gb:NM_002165.1 gb:D13889.1
203851_at	3.85	gb:NM_002178.1 /DEF=Homo sapiens insulin-like growth factor binding protein 6 (IGFBP6), mRNA. /FEA=mRNA /GEN=IGFBP6 /PROD=insulin-like growth factor binding protein 6 /DB_XREF=gi:11321592 /UG=Hs.274313 insulin-like growth factor binding protein 6 /FL=gb:NM_002178.1 gb:BC003507.1 gb:BC005007.1 gb:M62402.1
212551_at	3.84	Consensus includes gb:NM_006366.1 /DEF=Homo sapiens adenylyl cyclase-associated protein 2 (CAP2), mRNA. /FEA=CDS /GEN=CAP2 /PROD=adenylyl cyclase-associated protein 2 /DB_XREF=gi:5453592 /UG=Hs.296341 adenylyl cyclase-associated protein 2 /FL=gb:U02390.1 gb:NM_006366.1
201841_s_at	3.82	gb:NM_001540.2 /DEF=Homo sapiens heat shock 27kD protein 1 (HSPB1), mRNA. /FEA=mRNA /GEN=HSPB1 /PROD=heat shock 27kD protein 1 /DB_XREF=gi:4996892 /UG=Hs.76067 heat shock 27kD protein 1 /FL=gb:AB020027.1 gb:BC000510.1 gb:U90906.1 gb:NM_001540.2
203137_at	3.81	gb:NM_004906.1 /DEF=Homo sapiens Wilms tumour 1-associating protein (KIAA0105), mRNA. /FEA=mRNA /GEN=KIAA0105 /PROD=Wilms tumour 1-associating protein /DB_XREF=gi:4758635 /UG=Hs.119 Wilms tumour 1-associating protein /FL=gb:AF277190.1 gb:D14661.1 gb:NM_004906.1
200859_x_at	3.8	gb:NM_001456.1 /DEF=Homo sapiens filamin A, alpha (actin-binding protein-280) (FLNA), mRNA. /FEA=mRNA /GEN=FLNA /PROD=filamin 1 (actin-binding protein-280) /DB_XREF=gi:4503744 /UG=Hs.195464 filamin A, alpha (actin-binding protein-280) /FL=gb:NM_001456.1
203489_at	3.79	gb:NM_006427.2 /DEF=Homo sapiens CD27-binding (Siva) protein (SIVA), transcript variant 1, mRNA. /FEA=mRNA /GEN=SIVA /PROD=CD27-binding (Siva) protein isoform 1 /DB_XREF=gi:11277467 /UG=Hs.112058 CD27-binding (Siva) protein /FL=gb:NM_006427.2 gb:U82938.1
211501_s_at	3.77	gb:BC001173.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD), clone MGC:2051, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 3,subunit 9 (eta, 116kD) /DB_XREF=gi:12654668 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:BC001173.1

215223_s_at	3.76	Consensus includes gb:W46388 /FEA=EST /DB_XREF=gi:1331076 /DB_XREF=est:zc32c08.s1 /CLONE=IMAGE:324014 /UG=Hs.318885 superoxide dismutase 2, mitochondrial
209773_s_at	3.75	gb:BC001886.1 /DEF=Homo sapiens, ribonucleotide reductase M2 polypeptide, clone MGC:1551, mRNA, complete cds. /FEA=mRNA /PROD=ribonucleotide reductase M2 polypeptide /DB_XREF=gi:12804874 /UG=Hs.75319 ribonucleotide reductase M2 polypeptide /FL=gb:BC001886.1
203889_at	3.74	gb:NM_003020.1 /DEF=Homo sapiens secretory granule, neuroendocrine protein 1 (7B2 protein) (SGNE1), mRNA. /FEA=mRNA /GEN=SGNE1 /PROD=secretory granule, neuroendocrine protein 1 (7B2protein) /DB_XREF=gi:4506916 /UG=Hs.2265 secretory granule, neuroendocrine protein 1 (7B2 protein) /FL=gb:BC005349.1 gb:NM_003020.1
213524_s_at	3.74	Consensus includes gb:NM_015714.1 /DEF=Homo sapiens putative lymphocyte G0G1 switch gene (G0S2), mRNA. /FEA=CDS /GEN=G0S2 /PROD=putative lymphocyte G0G1 switch gene /DB_XREF=gi:7657103 /UG=Hs.95910 putative lymphocyte G0G1 switch gene /FL=gb:NM_015714.1
222037_at	3.73	Consensus includes gb:AI859865 /FEA=EST /DB_XREF=gi:5513481 /DB_XREF=est:wm21f03.x1 /CLONE=IMAGE:2436605 /UG=Hs.154443 minichromosome maintenance deficient (S. cerevisiae) 4
200613_at	3.72	gb:NM_004068.1 /DEF=Homo sapiens adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA. /FEA=mRNA /GEN=AP2M1 /PROD=adaptor-related protein complex 2, mu 1 subunit /DB_XREF=gi:4757993 /UG=Hs.152936 adaptor-related protein complex 2, mu 1 subunit /FL=gb:U36188.1 gb:BC004996.1 gb:D63475.1 gb:NM_004068.1
221269_s_at	3.71	gb:NM_031286.1 /DEF=Homo sapiens SH3BGRL3-like protein (SH3BGRL3), mRNA. /FEA=mRNA /GEN=SH3BGRL3 /PROD=SH3BGRL3-like protein /DB_XREF=gi:13775197 /FL=gb:NM_031286.1
211730_s_at	3.7	gb:BC005903.1 /DEF=Homo sapiens, polymerase (RNA) II (DNA directed) polypeptide L (7.6kD), clone MGC:14494, mRNA, complete cds. /FEA=mRNA /PROD=polymerase (RNA) II (DNA directed) polypeptide L(7.6kD) /DB_XREF=gi:13543491 /FL=gb:BC005903.1
214321_at	3.67	Consensus includes gb:BF440025 /FEA=EST /DB_XREF=gi:11452542 /DB_XREF=est:nac52c12.x1 /CLONE=IMAGE:3406079 /UG=Hs.235935 nephroblastoma overexpressed gene
217784_at	3.65	Consensus includes gb:BE384482 /FEA=EST /DB_XREF=gi:9329847 /DB_XREF=est:601277836F1 /CLONE=IMAGE:3618848 /UG=Hs.296244 SNARE protein /FL=gb:U95735.1 gb:NM_006555.1
205798_at	3.64	gb:NM_002185.1 /DEF=Homo sapiens interleukin 7 receptor (IL7R), mRNA. /FEA=mRNA /GEN=IL7R /PROD=interleukin 7 receptor /DB_XREF=gi:4504678 /UG=Hs.237868 interleukin 7 receptor /FL=gb:M29696.1 gb:NM_002185.1
212983_at	3.63	Consensus includes gb:NM_005343.1 /DEF=Homo sapiens v-Ha-ras Harvey rat sarcoma viral oncogene homolog (HRAS), mRNA. /FEA=CDS /GEN=HRAS /PROD=v-Ha-ras Harvey rat sarcoma viral oncogenehomolog /DB_XREF=gi:4885424 /UG=Hs.37003 v-Ha-ras Harvey rat sarcoma viral oncogene homolog /FL=gb:NM_005343.1
212691_at	3.63	Consensus includes gb:AW131863 /FEA=EST /DB_XREF=gi:6133470 /DB_XREF=est:xf35f02.x1 /CLONE=IMAGE:2620059 /UG=Hs.30002 SH3-containing protein SH3GLB2
215464_s_at	3.6	Consensus includes gb:AK001327.1 /DEF=Homo sapiens cDNA FLJ10465 fis, clone NT2RP1001616. /FEA=mRNA /DB_XREF=gi:7022515 /UG=Hs.12956 Tax interaction protein 1
202269_x_at	3.6	gb:BC002666.1 /DEF=Homo sapiens, guanylate binding protein 1, interferon-inducible, 67kD, clone MGC:3949, mRNA, complete cds. /FEA=mRNA /PROD=guanylate binding protein 1,interferon-inducible, 67kD /DB_XREF=gi:12803662 /UG=Hs.62661 guanylate binding protein 1, interferon-inducible, 67kD /FL=gb:BC002666.1 gb:M55542.1 gb:NM_002053.1
217875_s_at	3.56	gb:NM_020182.1 /DEF=Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), mRNA.

		/FEA=mRNA /GEN=TMEPAI /PROD=transmembrane, prostate androgen induced RNA /DB_XREF=gi:9910497 /UG=Hs.83883 transmembrane, prostate androgen induced RNA /FL=gb:AF224278.1 gb:NM_020182.1
204501_at	3.56	gb:NM_002514.1 /DEF=Homo sapiens nephroblastoma overexpressed gene (NOV), mRNA. /FEA=mRNA /GEN=NOV /PROD=nephroblastoma overexpressed gene /DB_XREF=gi:4505422 /UG=Hs.235935 nephroblastoma overexpressed gene /FL=gb:NM_002514.1
AFFX-r2-Hs28SrRNA-3_at	3.53	M11167 Human 28S rRNA sequence, length 5025 bases, middle target bases 1666-3330
209732_at	3.53	gb:BC005254.1 /DEF=Homo sapiens, Similar to C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced), clone MGC:12289, mRNA, complete cds. /FEA=mRNA /PROD=Similar to C-type (calcium dependent,carbohydrate-recognition domain) lectin, superfamilymember 2 (activation-induced) /DB_XREF=gi:13528920 /UG=Hs.85201 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) /FL=gb:BC005254.1 gb:AB015628.1 gb:NM_005127.1
218083_at	3.52	gb:NM_025072.1 /DEF=Homo sapiens hypothetical protein FLJ14038 (FLJ14038), mRNA. /FEA=mRNA /GEN=FLJ14038 /PROD=hypothetical protein FLJ14038 /DB_XREF=gi:13376616 /UG=Hs.288102 hypothetical protein FLJ14038 /FL=gb:NM_025072.1
202589_at	3.51	gb:NM_001071.1 /DEF=Homo sapiens thymidylate synthetase (TYMS), mRNA. /FEA=mRNA /GEN=TYMS /PROD=thymidylate synthetase /DB_XREF=gi:4507750 /UG=Hs.82962 thymidylate synthetase /FL=gb:BC002567.1 gb:NM_001071.1
212680_x_at	3.5	Consensus includes gb:BE305165 /FEA=EST /DB_XREF=gi:9177184 /DB_XREF=est:601186685T1 /CLONE=IMAGE:2959580 /UG=Hs.100623 phospholipase C, beta 3, neighbor pseudogene
212218_s_at	3.44	Consensus includes gb:AI954041 /FEA=EST /DB_XREF=gi:5746351 /DB_XREF=est:wx78h04.x1 /CLONE=IMAGE:2549815 /UG=Hs.11050 F-box only protein 9 /FL=gb:NM_012347.1
203571_s_at	3.43	gb:NM_006829.1 /DEF=Homo sapiens adipose specific 2 (APM2), mRNA. /FEA=mRNA /GEN=APM2 /PROD=adipose specific 2 /DB_XREF=gi:5802975 /UG=Hs.74120 adipose specific 2 /FL=gb:BC004471.1 gb:NM_006829.1 gb:D45370.1
204141_at	3.42	gb:NM_001069.1 /DEF=Homo sapiens tubulin, beta polypeptide (TUBB), mRNA. /FEA=mRNA /GEN=TUBB /PROD=tubulin, beta polypeptide /DB_XREF=gi:4507728 /UG=Hs.179661 tubulin, beta polypeptide /FL=gb:BC001194.1 gb:NM_001069.1
201264_at	3.42	gb:NM_007263.1 /DEF=Homo sapiens coatomer protein complex, subunit epsilon (COPE), mRNA. /FEA=mRNA /GEN=COPE /PROD=coatomer protein complex, subunit epsilon /DB_XREF=gi:6005734 /UG=Hs.10326 coatomer protein complex, subunit epsilon /FL=gb:AL136928.1 gb:BC003155.1 gb:NM_007263.1
205207_at	3.42	gb:NM_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6 /PROD=interleukin 6 (interferon, beta 2) /DB_XREF=gi:10834983 /UG=Hs.93913 interleukin 6 (interferon, beta 2) /FL=gb:NM_000600.1 gb:M14584.1 gb:M18403.1 gb:M29150.1 gb:M54894.1
202644_s_at	3.41	gb:NM_006290.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA. /FEA=mRNA /GEN=TNFAIP3 /PROD=tumor necrosis factor, alpha-induced protein 3 /DB_XREF=gi:5454131 /UG=Hs.211600 tumor necrosis factor, alpha-induced protein 3 /FL=gb:M59465.1 gb:NM_006290.1
209427_at	3.41	gb:AF064238.3 /DEF=Homo sapiens smoothelin large isoform L2 (SMTN) mRNA, complete cds. /FEA=mRNA /GEN=SMTN /PROD=smoothelin large isoform L2 /DB_XREF=gi:8119287 /UG=Hs.149098 smoothelin /FL=gb:AF064238.3
201040_at	3.41	gb:NM_002070.1 /DEF=Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GNAI2), mRNA. /FEA=mRNA /GEN=GNAI2 /PROD=guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 2 /DB_XREF=gi:4504040 /UG=Hs.77269 guanine nucleotide binding

		protein (G protein), alpha inhibiting activity polypeptide 2 /FL=gb:J03004.1 gb:NM_002070.1
206421_s_at	3.4	gb:NM_003784.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 (SERPINB7), mRNA. /FEA=mRNA /GEN=SERPINB7 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 7 /DB_XREF=gi:4505148 /UG=Hs.138202 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 /FL=gb:AF027866.1 gb:NM_003784.1
214146_s_at	3.4	Consensus includes gb:R64130 /FEA=EST /DB_XREF=gi:836009 /DB_XREF=est:yi18h03.s1 /CLONE=IMAGE:139637 /UG=Hs.2164 pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
217025_s_at	3.4	Consensus includes gb:AL110225.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D064 (from clone DKFZp434D064); partial cds. /FEA=mRNA /GEN=DKFZp434D064 /PROD=hypothetical protein /DB_XREF=gi:5817161 /UG=Hs.89434 drebrin 1
214752_x_at	3.39	Consensus includes gb:AI625550 /FEA=EST /DB_XREF=gi:4650481 /DB_XREF=est:ty57d06.x1 /CLONE=IMAGE:2283179 /UG=Hs.195464 filamin A, alpha (actin-binding protein-280)
1861_at	3.39	U66879 /FEATURE= /DEFINITION=HSU66879 Human Bcl-2 binding component 6 (bbc6) mRNA, complete cds
211906_s_at	3.37	gb:AB046400.1 /DEF=Homo sapiens mRNA for SCCA2b, complete cds. /FEA=CDS /GEN=SCCA2 /PROD=SCCA2b /DB_XREF=gi:13537193 /FL=gb:AB046400.1
212977_at	3.37	Consensus includes gb:AI817041 /FEA=EST /DB_XREF=gi:5436120 /DB_XREF=est:wj76c06.x1 /CLONE=IMAGE:2408746 /UG=Hs.23016 G protein-coupled receptor
221805_at	3.35	Consensus includes gb:AL537457 /FEA=EST /DB_XREF=gi:12800950 /DB_XREF=est:AL537457 /CLONE=CS0DF025YH07 (3 prime) /UG=Hs.211584 neurofilament, light polypeptide (68kD) /FL=gb:NM_006158.1
212877_at	3.33	Consensus includes gb:AA284075 /FEA=EST /DB_XREF=gi:1928356 /DB_XREF=est:zs49b01.s1 /CLONE=IMAGE:700777 /UG=Hs.117977 kinesin 2 (60-70kD)
210285_x_at	3.32	gb:BC000383.1 /DEF=Homo sapiens, Wilms tumour 1-associating protein, clone MGC:8419, mRNA, complete cds. /FEA=mRNA /PROD=Wilms tumour 1-associating protein /DB_XREF=gi:12653228 /UG=Hs.119 Wilms tumour 1-associating protein /FL=gb:BC000383.1 gb:BC004432.1
203252_at	3.32	gb:NM_005851.1 /DEF=Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R), mRNA. /FEA=mRNA /GEN=DOC-1R /PROD=tumor suppressor deleted in oral cancer-related1 /DB_XREF=gi:5031668 /UG=Hs.25664 tumor suppressor deleted in oral cancer-related 1 /FL=gb:BC002850.1 gb:AF089814.1 gb:NM_005851.1
209720_s_at	3.31	gb:BC005224.1 /DEF=Homo sapiens, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3, clone MGC:12244, mRNA, complete cds. /FEA=mRNA /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 3 /DB_XREF=gi:13528851 /UG=Hs.227948 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3 /FL=gb:U19556.1 gb:BC005224.1 gb:NM_006919.1
212540_at	3.3	Consensus includes gb:BG476661 /FEA=EST /DB_XREF=gi:13408940 /DB_XREF=est:602524946F1 /CLONE=IMAGE:4643458 /UG=Hs.76932 cell division cycle 34
202107_s_at	3.3	gb:NM_004526.1 /DEF=Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) (MCM2), mRNA. /FEA=mRNA /GEN=MCM2 /PROD=minichromosome maintenance deficient (S.cerevisiae) 2 (mitotin) /DB_XREF=gi:4758705 /UG=Hs.57101 minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) /FL=gb:D83987.1 gb:NM_004526.1
216952_s_at	3.29	Consensus includes gb:M94363 /DEF=Human lamin B2 (LAMB2) gene and ppv1 gene sequence /FEA=mRNA /DB_XREF=gi:186920 /UG=Hs.76084 lamin B2
204767_s_at	3.27	gb:BC000323.1 /DEF=Homo sapiens, flap structure-specific endonuclease 1, clone MGC:8478, mRNA, complete cds. /FEA=mRNA /PROD=flap structure-specific endonuclease 1 /DB_XREF=gi:12653112 /UG=Hs.4756 flap

		structure-specific endonuclease 1 /FL=gb:BC000323.1 gb:NM_004111.3
201890_at	3.27	Consensus includes gb:BE966236 /FEA=EST /DB_XREF=gi:11771437 /DB_XREF=est:601660172R1 /CLONE=IMAGE:3905920 /UG=Hs.75319 ribonucleotide reductase M2 polypeptide /FL=gb:NM_001034.1
216237_s_at	3.26	Consensus includes gb:AA807529 /FEA=EST /DB_XREF=gi:2875596 /DB_XREF=est:ob92c07.s1 /CLONE=IMAGE:1338828 /UG=Hs.77171 minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46)
212188_at	3.26	Consensus includes gb:AA551075 /FEA=EST /DB_XREF=gi:2321327 /DB_XREF=est:nk74h06.s1 /CLONE=IMAGE:1019291 /UG=Hs.109438 Homo sapiens clone 24775 mRNA sequence
217782_s_at	3.25	gb:NM_004127.3 /DEF=Homo sapiens G protein pathway suppressor 1 (GPS1), mRNA. /FEA=mRNA /GEN=GPS1 /PROD=G protein pathway suppressor 1 /DB_XREF=gi:13435380 /UG=Hs.268530 G protein pathway suppressor 1 /FL=gb:BC000155.1 gb:NM_004127.3 gb:U20285.2
218952_at	3.23	gb:NM_013271.1 /DEF=Homo sapiens granin-like neuroendocrine peptide precursor (SAAS), mRNA. /FEA=mRNA /GEN=SAAS /PROD=granin-like neuroendocrine peptide precursor /DB_XREF=gi:7019518 /UG=Hs.256311 granin-like neuroendocrine peptide precursor /FL=gb:BC002851.1 gb:AF181562.1 gb:NM_013271.1
205681_at	3.22	gb:NM_004049.1 /DEF=Homo sapiens BCL2-related protein A1 (BCL2A1), mRNA. /FEA=mRNA /GEN=BCL2A1 /PROD=BCL2-related protein A1 /DB_XREF=gi:4757839 /UG=Hs.227817 BCL2-related protein A1 /FL=gb:U27467.1 gb:U29680.1 gb:NM_004049.1
204337_at	3.21	Consensus includes gb:AL514445 /FEA=EST /DB_XREF=gi:12777939 /DB_XREF=est:AL514445 /CLONE=CL0BB010ZF08 (3 prime) /UG=Hs.227571 regulator of G-protein signalling 4 /FL=gb:NM_005613.2 gb:BC000737.1
208782_at	3.21	gb:BC000055.1 /DEF=Homo sapiens, follistatin-like 1, clone MGC:1993, mRNA, complete cds. /FEA=mRNA /PROD=follistatin-like 1 /DB_XREF=gi:12652618 /UG=Hs.296267 follistatin-like 1 /FL=gb:BC000055.1 gb:U06863.1
202912_at	3.2	gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mRNA /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 /UG=Hs.394 adrenomedullin /FL=gb:NM_001124.1 gb:D14874.1
203967_at	3.2	gb:U77949.1 /DEF=Human Cdc6-related protein (HsCDC6) mRNA, complete cds. /FEA=mRNA /GEN=HsCDC6 /PROD=Cdc6-related protein /DB_XREF=gi:1684902 /UG=Hs.69563 CDC6 (cell division cycle 6, S. cerevisiae) homolog /FL=gb:U77949.1 gb:AF022109.1 gb:NM_001254.1
216442_x_at	3.19	Consensus includes gb:AK026737.1 /DEF=Homo sapiens cDNA: FLJ23084 fis, clone LNG06602, highly similar to HSFIB1 Human mRNA for fibronectin (FN precursor). /FEA=mRNA /DB_XREF=gi:10439658 /UG=Hs.287820 fibronectin 1
205082_s_at	3.18	gb:AB046692.1 /DEF=Homo sapiens hAO mRNA for aldeyde oxidase, complete cds. /FEA=mRNA /GEN=hAO /PROD=aldeyde oxidase /DB_XREF=gi:13516378 /UG=Hs.174151 aldehyde oxidase 1 /FL=gb:AB046692.1 gb:L11005.1 gb:NM_001159.2
209277_at	3.18	Consensus includes gb:AL574096 /FEA=EST /DB_XREF=gi:12933969 /DB_XREF=est:AL574096 /CLONE=CS0DI040YI17 (3 prime) /UG=Hs.295944 tissue factor pathway inhibitor 2 /FL=gb:BC005330.1 gb:L27624.1 gb:D29992.1 gb:NM_006528.1
205034_at	3.17	gb:NM_004702.1 /DEF=Homo sapiens cyclin E2 (CCNE2), mRNA. /FEA=mRNA /GEN=CCNE2 /PROD=cyclin E2 /DB_XREF=gi:4757931 /UG=Hs.30464 cyclin E2 /FL=gb:AF091433.1 gb:AF102778.1 gb:AF106690.1 gb:NM_004702.1
209026_x_at	3.17	gb:AF141349.1 /DEF=Homo sapiens beta-tubulin mRNA, complete cds. /FEA=mRNA /PROD=beta-tubulin /DB_XREF=gi:4929137 /UG=Hs.179661 tubulin, beta polypeptide /FL=gb:BC000222.1 gb:BC002347.1 gb:BC001938.1 gb:AF070561.1 gb:AF070593.1 gb:AF070600.1 gb:AF141349.1
206924_at	3.15	gb:NM_000641.1 /DEF=Homo sapiens interleukin 11 (IL11), mRNA. /FEA=mRNA /GEN=IL11 /PROD=interleukin

		11 /DB_XREF=gi:10834993 /UG=Hs.1721 interleukin 11 /FL=gb:NM_000641.1 gb:M57765.1
205024_s_at	3.15	gb:NM_002875.1 /DEF=Homo sapiens RAD51 (S. cerevisiae) homolog (E coli RecA homolog) (RAD51), mRNA. /FEA=mRNA /GEN=RAD51 /PROD=RAD51 (S. cerevisiae) homolog (E coli RecAhomolog) /DB_XREF=gi:4506388 /UG=Hs.23044 RAD51 (S. cerevisiae) homolog (E coli RecA homolog) /FL=gb:D14134.1 gb:D13804.1 gb:NM_002875.1
218695_at	3.14	gb:NM_019037.1 /DEF=Homo sapiens hypothetical protein (FLJ20591), mRNA. /FEA=mRNA /GEN=FLJ20591 /PROD=hypothetical protein /DB_XREF=gi:9506688 /UG=Hs.97574 exosome component Rrp41 /FL=gb:BC002777.1 gb:AF281133.1 gb:NM_019037.1
201392_s_at	3.13	Consensus includes gb:BG031974 /FEA=EST /DB_XREF=gi:12422804 /DB_XREF=est:602300668F1 /CLONE=IMAGE:4402217 /UG=Hs.76473 insulin-like growth factor 2 receptor /FL=gb:J03528.1 gb:NM_000876.1
204619_s_at	3.13	Consensus includes gb:BF590263 /FEA=EST /DB_XREF=gi:11682587 /DB_XREF=est:nab22b12.x1 /CLONE=IMAGE:3266638 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican) /FL=gb:NM_004385.1
91684_g_at	3.11	Cluster Incl. AI571298:tn44e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2170492 /clone_end=3 /gb=AI571298 /gi=4534672 /ug=Hs.97574 /len=537
200075_s_at	3.08	gb:BC006249.1 /DEF=Homo sapiens, guanylate kinase 1, clone MGC:10618, mRNA, complete cds. /FEA=mRNA /PROD=guanylate kinase 1 /DB_XREF=gi:13623296 /FL=gb:BC006249.1
202998_s_at	3.07	gb:NM_002318.1 /DEF=Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /FEA=mRNA /GEN=LOXL2 /PROD=lysyl oxidase-like 2 /DB_XREF=gi:4505010 /UG=Hs.83354 lysyl oxidase-like 2 /FL=gb:BC000594.1 gb:U89942.1 gb:NM_002318.1 gb:AF117949.1
220651_s_at	3.07	gb:NM_018518.1 /DEF=Homo sapiens homolog of yeast MCM10; hypothetical protein PRO2249 (PRO2249), mRNA. /FEA=mRNA /GEN=PRO2249 /PROD=homolog of yeast MCM10; hypothetical proteinPRO2249 /DB_XREF=gi:8924142 /UG=Hs.198363 homolog of yeast MCM10; hypothetical protein PRO2249 /FL=gb:AB042719.1 gb:BC004876.1 gb:AF119869.1 gb:NM_018518.1
203931_s_at	3.07	gb:NM_002949.1 /DEF=Homo sapiens mitochondrial ribosomal protein L12 (MRPL12), mRNA. /FEA=mRNA /GEN=MRPL12 /PROD=mitochondrial ribosomal protein L12 /DB_XREF=gi:4506672 /UG=Hs.109059 mitochondrial ribosomal protein L12 /FL=gb:BC002344.1 gb:U25041.1 gb:AF105278.1 gb:NM_002949.1
217849_s_at	3.05	gb:NM_006035.1 /DEF=Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA. /FEA=mRNA /GEN=CDC42BPB /PROD=CDC42-binding protein kinase beta (DMPK-like) /DB_XREF=gi:5174412 /UG=Hs.12908 CDC42-binding protein kinase beta (DMPK-like) /FL=gb:AF128625.1 gb:NM_006035.1
204647_at	3.05	gb:NM_004838.1 /DEF=Homo sapiens Homer, neuronal immediate early gene, 3 (HOMER-3), mRNA. /FEA=mRNA /GEN=HOMER-3 /PROD=Homer, neuronal immediate early gene, 3 /DB_XREF=gi:4758549 /UG=Hs.166146 Homer, neuronal immediate early gene, 3 /FL=gb:AF093265.1 gb:NM_004838.1
210495_x_at	3.05	gb:AF130095.1 /DEF=Homo sapiens clone FLC0562 PRO2841 mRNA, complete cds. /FEA=mRNA /PROD=PRO2841 /DB_XREF=gi:11493493 /UG=Hs.287820 fibronectin 1 /FL=gb:AF130095.1
213520_at	3.04	Consensus includes gb:NM_004260.1 /DEF=Homo sapiens RecQ protein-like 4 (RECQL4), mRNA. /FEA=CDS /GEN=RECQL4 /PROD=RecQ protein-like 4 /DB_XREF=gi:4759029 /UG=Hs.31442 RecQ protein-like 4 /FL=gb:AB006532.1 gb:NM_004260.1
211571_s_at	3.04	gb:D32039.1 /DEF=Human pgH3 mRNA for proteoglycan PG-M(V3), complete cds. /FEA=mRNA /GEN=pgH3 /PROD=proteoglycan PG-M(V3) /DB_XREF=gi:1008912 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican) /FL=gb:D32039.1
218532_s_at	3.04	gb:NM_019000.1 /DEF=Homo sapiens hypothetical protein (FLJ20152), mRNA. /FEA=mRNA /GEN=FLJ20152 /PROD=hypothetical protein /DB_XREF=gi:9506660 /UG=Hs.82273 hypothetical protein /FL=gb:NM_019000.1
45633_at	3.03	Cluster Incl. AI421812:tf55a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2103156 /clone_end=3

		/gb=AI421812 /gi=4267743 /ug=Hs.47125 /len=556
215078_at	3.01	Consensus includes gb:AL050388.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds. /FEA=mRNA /GEN=DKFZp564M2422 /PROD=hypothetical protein /DB_XREF=gi:4914612 /UG=Hs.306320 Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds
203109_at	3.01	gb:NM_003969.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2M (homologous to yeast UBC12) (UBE2M), mRNA. /FEA=mRNA /GEN=UBE2M /PROD=ubiquitin-conjugating enzyme E2M (homologous toyeast UBC12) /DB_XREF=gi:4507790 /UG=Hs.200478 ubiquitin-conjugating enzyme E2M (homologous to yeast UBC12) /FL=gb:AF075599.1 gb:AB012191.1 gb:NM_003969.1
201426_s_at	3	Consensus includes gb:AI922599 /FEA=EST /DB_XREF=gi:5658563 /DB_XREF=est:wm90b11.x1 /CLONE=IMAGE:2443197 /UG=Hs.297753 vimentin /FL=gb:BC000163.2 gb:NM_003380.1
221247_s_at	3	gb:NM_030798.1 /DEF=Homo sapiens hypothetical protein DKFZp434D0421 (DKFZP434D0421), mRNA. /FEA=mRNA /GEN=DKFZP434D0421 /PROD=hypothetical protein DKFZp434D0421 /DB_XREF=gi:13540581 /FL=gb:NM_030798.1
215735_s_at	3	Consensus includes gb:AC005600 /DEF=Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence /FEA=CDS_1 /DB_XREF=gi:3522919 /UG=Hs.90303 tuberous sclerosis 2
202208_s_at	3	gb:BC001051.1 /DEF=Homo sapiens, ADP-ribosylation factor-like 7, clone MGC:1575, mRNA, complete cds. /FEA=mRNA /PROD=ADP-ribosylation factor-like 7 /DB_XREF=gi:12654450 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
AFFX-HUMRGE/M10098_M_at	3	M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
201079_at	2.98	gb:NM_004710.1 /DEF=Homo sapiens synaptogyrin 2 (SYNGR2), mRNA. /FEA=mRNA /GEN=SYNGR2 /PROD=synaptogyrin 2 /DB_XREF=gi:4759201 /UG=Hs.5097 synaptogyrin 2 /FL=gb:BC000407.1 gb:NM_004710.1
200678_x_at	2.98	gb:NM_002087.1 /DEF=Homo sapiens granulin (GRN), mRNA. /FEA=mRNA /GEN=GRN /PROD=granulin /DB_XREF=gi:4504150 /UG=Hs.180577 granulin /FL=gb:M75161.1 gb:AF055008.1 gb:NM_002087.1
211136_s_at	2.98	gb:BC004865.1 /DEF=Homo sapiens, cleft lip and palate associated transmembrane protein 1, clone MGC:10593, mRNA, complete cds. /FEA=mRNA /PROD=cleft lip and palate associated transmembraneprotein 1 /DB_XREF=gi:13436079 /UG=Hs.106671 cleft lip and palate associated transmembrane protein 1 /FL=gb:BC004865.1
221657_s_at	2.97	gb:BC001719.1 /DEF=Homo sapiens, Similar to hypothetical protein FLJ20548, clone MGC:1024, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein FLJ20548 /DB_XREF=gi:12804594 /UG=Hs.125037 hypothetical protein FLJ20548 /FL=gb:BC001719.1
213906_at	2.97	Consensus includes gb:AW592266 /FEA=EST /DB_XREF=gi:7279443 /DB_XREF=est:hf48e04.x1 /CLONE=IMAGE:2935134 /UG=Hs.300592 v-myb avian myeloblastosis viral oncogene homolog-like 1
217871_s_at	2.96	gb:NM_002415.1 /DEF=Homo sapiens macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA. /FEA=mRNA /GEN=MIF /PROD=macrophage migration inhibitory factor(glycosylation-inhibiting factor) /DB_XREF=gi:4505184 /UG=Hs.73798 macrophage migration inhibitory factor (glycosylation-inhibiting factor) /FL=gb:BC000447.1 gb:M25639.1 gb:L10612.1 gb:NM_002415.1
204236_at	2.96	gb:NM_002017.2 /DEF=Homo sapiens Friend leukemia virus integration 1 (FLI1), mRNA. /FEA=mRNA /GEN=FLI1 /PROD=Friend leukemia virus integration 1 /DB_XREF=gi:7110592 /UG=Hs.108043 Friend leukemia virus integration 1 /FL=gb:BC001670.1 gb:M98833.3 gb:NM_002017.2

214426_x_at	2.94	Consensus includes gb:BF062223 /FEA=EST /DB_XREF=gi:10821121 /DB_XREF=est:7k74c04.x1 /CLONE=IMAGE:3480967 /UG=Hs.79018 chromatin assembly factor 1, subunit A (p150)
211714_x_at	2.94	gb:BC005838.1 /DEF=Homo sapiens, tubulin, beta 5, clone MGC:2440, mRNA, complete cds. /FEA=mRNA /PROD=tubulin, beta 5 /DB_XREF=gi:13543349 /FL=gb:BC005838.1
219588_s_at	2.92	gb:NM_017760.1 /DEF=Homo sapiens hypothetical protein FLJ20311 (FLJ20311), mRNA. /FEA=mRNA /GEN=FLJ20311 /PROD=hypothetical protein FLJ20311 /DB_XREF=gi:8923292 /UG=Hs.18616 hypothetical protein FLJ20311 /FL=gb:NM_017760.1
211716_x_at	2.92	gb:BC005851.1 /DEF=Homo sapiens, Rho GDP dissociation inhibitor (GDI) alpha, clone MGC:2810, mRNA, complete cds. /FEA=mRNA /PROD=Rho GDP dissociation inhibitor (GDI) alpha /DB_XREF=gi:13543380 /FL=gb:BC005851.1
204462_s_at	2.92	gb:NM_006517.1 /DEF=Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transporter) (SLC16A2), mRNA. /FEA=mRNA /GEN=SLC16A2 /PROD=solute carrier family 16 (monocarboxylic acidtransporters), member 2 (putative transporter) /DB_XREF=gi:5730044 /UG=Hs.75317 solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transporter) /FL=gb:NM_006517.1
209706_at	2.92	gb:AF247704.1 /DEF=Homo sapiens homeobox protein NKX3.1 mRNA, complete cds. /FEA=mRNA /PROD=homeobox protein NKX3.1 /DB_XREF=gi:9963969 /UG=Hs.55999 NK homeobox (Drosophila), family 3, A /FL=gb:AF249670.1 gb:AF249672.1 gb:U80669.1 gb:U91540.1 gb:NM_006167.1 gb:AF247704.1
202014_at	2.91	gb:NM_014330.2 /DEF=Homo sapiens growth arrest and DNA-damage-inducible 34 (GADD34), mRNA. /FEA=mRNA /GEN=GADD34 /PROD=growth arrest and DNA-damage-inducible 34 /DB_XREF=gi:9790902 /UG=Hs.76556 growth arrest and DNA-damage-inducible 34 /FL=gb:BC003067.1 gb:U83981.1 gb:NM_014330.2
207891_s_at	2.91	gb:NM_017518.2 /DEF=Homo sapiens Xq28, 2000bp sequence contg. ORF (HSXQ28ORF), mRNA. /FEA=mRNA /GEN=HSXQ28ORF /PROD=Xq28, 2000bp sequence contg. ORF /DB_XREF=gi:11120679 /UG=Hs.6487 Xq28, 2000bp sequence contg. ORF /FL=gb:NM_017518.2 gb:AF267739.1
221916_at	2.9	Consensus includes gb:BF055311 /FEA=EST /DB_XREF=gi:10809207 /DB_XREF=est:7j78a07.x1 /CLONE=IMAGE:3392532 /UG=Hs.302689 hypothetical protein
218875_s_at	2.9	gb:NM_012177.1 /DEF=Homo sapiens F-box only protein 5 (FBXO5), mRNA. /FEA=mRNA /GEN=FBXO5 /PROD=F-box only protein 5 /DB_XREF=gi:6912365 /UG=Hs.272027 F-box only protein 5 /FL=gb:AF129535.1 gb:NM_012177.1
205035_at	2.9	gb:NM_004715.1 /DEF=Homo sapiens CTD (carboxy-terminal domina, RNA polymerase II, polypeptide A) phosphatase, subunit 1 (CTDP1), mRNA. /FEA=mRNA /GEN=CTDP1 /PROD=CTD (carboxy-terminal domina, RNA polymerase II,polypeptide A) phosphatase, subunit 1 /DB_XREF=gi:4758093 /UG=Hs.4076 CTD (carboxy-terminal domina, RNA polymerase II, polypeptide A) phosphatase, subunit 1 /FL=gb:AF081287.1 gb:NM_004715.1 gb:AF154115.1
201331_s_at	2.9	gb:BC004973.1 /DEF=Homo sapiens, signal transducer and activator of transcription 6, interleukin-4 induced, clone MGC:3649, mRNA, complete cds. /FEA=mRNA /PROD=signal transducer and activator of transcription6, interleukin-4 induced /DB_XREF=gi:13436385 /UG=Hs.181015 signal transducer and activator of transcription 6, interleukin-4 induced /FL=gb:BC004973.1 gb:NM_003153.1 gb:U16031.1
205436_s_at	2.89	gb:NM_002105.1 /DEF=Homo sapiens H2A histone family, member X (H2AFX), mRNA. /FEA=mRNA /GEN=H2AFX /PROD=H2A histone family, member X /DB_XREF=gi:4504252 /UG=Hs.147097 H2A histone family, member X /FL=gb:BC004915.1 gb:NM_002105.1
213187_x_at	2.87	Consensus includes gb:BG538564 /FEA=EST /DB_XREF=gi:13530797 /DB_XREF=est:602567289F1 /CLONE=IMAGE:4691639 /UG=Hs.324746 alpha-2-HS-glycoprotein
204603_at	2.86	gb:NM_003686.1 /DEF=Homo sapiens exonuclease 1 (EXO1), mRNA. /FEA=mRNA /GEN=EXO1 /PROD=Rad2

		nuclease family member, homolog of S.cerevisiae exonuclease 1 /DB_XREF=gi:4504368 /UG=Hs.47504 exonuclease 1 /FL=gb:NM_006027.1 gb:AF042282.1 gb:AF060479.1 gb:AF091740.1 gb:AF084974.1 gb:NM_003686.1
204768_s_at	2.84	gb:NM_004111.3 /DEF=Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA. /FEA=mRNA /GEN=FEN1 /PROD=flap structure-specific endonuclease 1 /DB_XREF=gi:6325465 /UG=Hs.4756 flap structure-specific endonuclease 1 /FL=gb:BC000323.1 gb:NM_004111.3
220615_s_at	2.84	gb:NM_018099.1 /DEF=Homo sapiens hypothetical protein FLJ10462 (FLJ10462), mRNA. /FEA=mRNA /GEN=FLJ10462 /PROD=hypothetical protein FLJ10462 /DB_XREF=gi:8922433 /UG=Hs.100895 hypothetical protein FLJ10462 /FL=gb:AL136843.1 gb:NM_018099.1
211168_s_at	2.82	gb:D86988.1 /DEF=Human mRNA for KIAA0221 gene, complete cds. /FEA=mRNA /GEN=KIAA0221 /PROD=KIAA0221 /DB_XREF=gi:1944406 /UG=Hs.12719 regulator of nonsense transcripts 1 /FL=gb:D86988.1
31874_at	2.81	Cluster Incl. Y07846:H.sapiens mRNA for GAR22 protein /cds=(132,1145) /gb=Y07846 /gi=1666070 /ug=Hs.15346 /len=2238
211006_s_at	2.81	gb:L02840.1 /DEF=Homo sapiens potassium channel Kv2.1 mRNA, complete cds. /FEA=mRNA /PROD=voltage-gated potassium channel /DB_XREF=gi:186797 /UG=Hs.84244 potassium voltage-gated channel, Shab-related subfamily, member 1 /FL=gb:L02840.1 gb:AF026005.1 gb:NM_004975.1
203718_at	2.8	gb:NM_006702.1 /DEF=Homo sapiens neuropathy target esterase (NTE), mRNA. /FEA=mRNA /GEN=NTE /PROD=neuropathy target esterase /DB_XREF=gi:5729950 /UG=Hs.5038 neuropathy target esterase /FL=gb:NM_006702.1
200852_x_at	2.8	gb:NM_005273.1 /DEF=Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 2 (GNB2), mRNA. /FEA=mRNA /GEN=GNB2 /PROD=guanine nucleotide binding protein (G protein),beta polypeptide 2 /DB_XREF=gi:4885282 /UG=Hs.91299 guanine nucleotide binding protein (G protein), beta polypeptide 2 /FL=gb:M16538.1 gb:M36429.1 gb:NM_005273.1
209665_at	2.8	gb:AF040704.1 /DEF=Homo sapiens putative tumor suppressor protein (101F6) mRNA, complete cds. /FEA=mRNA /GEN=101F6 /PROD=putative tumor suppressor protein /DB_XREF=gi:2935319 /UG=Hs.149443 putative tumor suppressor /FL=gb:AF040704.1 gb:NM_007022.1
202270_at	2.8	gb:NM_002053.1 /DEF=Homo sapiens guanylate binding protein 1, interferon-inducible, 67kD (GBP1), mRNA. /FEA=mRNA /GEN=GBP1 /PROD=guanylate binding protein 1,interferon-inducible, 67kD /DB_XREF=gi:4503938 /UG=Hs.62661 guanylate binding protein 1, interferon-inducible, 67kD /FL=gb:BC002666.1 gb:M55542.1 gb:NM_002053.1
202071_at	2.79	gb:NM_002999.1 /DEF=Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4), mRNA. /FEA=mRNA /GEN=SDC4 /PROD=syndecan 4 (amphiglycan, ryudocan) /DB_XREF=gi:4506860 /UG=Hs.252189 syndecan 4 (amphiglycan, ryudocan) /FL=gb:NM_002999.1
212636_at	2.79	Consensus includes gb:AL031781 /DEF=Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3 part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Con... /FEA=mRNA_2 /DB_XREF=gi:4038570 /UG=Hs.15020 homolog of mouse quaking QKI (KH domain RNA binding protein) /FL=gb:AF142417.1
213977_s_at	2.79	Consensus includes gb:AA054734 /FEA=EST /DB_XREF=gi:1545679 /DB_XREF=est:zk68f07.s1 /CLONE=IMAGE:488005 /UG=Hs.23476 Cip1-interacting zinc finger protein
201700_at	2.78	gb:NM_001760.1 /DEF=Homo sapiens cyclin D3 (CCND3), mRNA. /FEA=mRNA /GEN=CCND3 /PROD=cyclin D3 /DB_XREF=gi:4502618 /UG=Hs.83173 cyclin D3 /FL=gb:M90814.1 gb:M92287.1 gb:NM_001760.1
200766_at	2.78	gb:NM_001909.1 /DEF=Homo sapiens cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA. /FEA=mRNA

		/GEN=CTSD /PROD=cathepsin D (lysosomal aspartyl protease) /DB_XREF=gi:4503142 /UG=Hs.79572 cathepsin D (lysosomal aspartyl protease) /FL=gb:M11233.1 gb:NM_001909.1
212646_at	2.78	Consensus includes gb:D42043.1 /DEF=Human mRNA for KIAA0084 gene, partial cds. /FEA=mRNA /GEN=KIAA0084 /DB_XREF=gi:577298 /UG=Hs.79123 KIAA0084 protein
213040_s_at	2.78	Consensus includes gb:AL008583 /DEF=Human DNA sequence from clone RP3-327J16 on chromosome 22q12.3-13.2 Contains the DNAL4 gene for axonemal dynein light polypeptide 4, the NPTXR gene for neuronal pentraxin receptor and the CBX6 gene for chromobox homolog 6. Contains ESTs, STSs, a G... /FEA=mRNA_2 /DB_XREF=gi:4160195 /UG=Hs.91622 neuronal pentraxin receptor /FL=gb:NM_014293.1
52741_at	2.77	Cluster Incl. AI962879:wt24c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2508394 /clone_end=3 /gb=AI962879 /gi=5755592 /ug=Hs.81920 /len=490
208791_at	2.77	gb:M25915.1 /DEF=Human complement cytolysis inhibitor (CLI) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:180619 /UG=Hs.75106 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) /FL=gb:J02908.1 gb:M25915.1 gb:M64722.1 gb:NM_001831.1
214383_x_at	2.77	Consensus includes gb:BF063121 /FEA=EST /DB_XREF=gi:10822031 /DB_XREF=est:7h83f11.x1 /CLONE=IMAGE:3322605 /UG=Hs.281706 sortilin 1
206953_s_at	2.76	gb:NM_012302.1 /DEF=Homo sapiens latrophilin (KIAA0786), mRNA. /FEA=mRNA /GEN=KIAA0786 /PROD=latrophilin /DB_XREF=gi:6912463 /UG=Hs.24212 latrophilin /FL=gb:AF104939.1 gb:NM_012302.1
208711_s_at	2.76	gb:BC000076.1 /DEF=Homo sapiens, cyclin D1 (PRAD1: parathyroid adenomatosis 1), clone MGC:2316, mRNA, complete cds. /FEA=mRNA /PROD=cyclin D1 (PRAD1: parathyroid adenomatosis 1) /DB_XREF=gi:12652656 /UG=Hs.82932 cyclin D1 (PRAD1: parathyroid adenomatosis 1) /FL=gb:BC000076.1 gb:M73554.1
204727_at	2.76	Consensus includes gb:AW772140 /FEA=EST /DB_XREF=gi:7704203 /DB_XREF=est:hn68b03.x1 /CLONE=IMAGE:3033005 /UG=Hs.72160 AND-1 protein /FL=gb:NM_007086.1
209729_at	2.75	gb:BC001782.1 /DEF=Homo sapiens, GAS2-related on chromosome 22, clone MGC:2104, mRNA, complete cds. /FEA=mRNA /PROD=GAS2-related on chromosome 22 /DB_XREF=gi:12804706 /UG=Hs.322852 Homo sapiens, GAS2-related on chromosome 22, clone MGC:2104, mRNA, complete cds /FL=gb:BC001782.1
213726_x_at	2.75	Consensus includes gb:AA515698 /FEA=EST /DB_XREF=gi:2255298 /DB_XREF=est:nf66f09.s1 /CLONE=IMAGE:924905 /UG=Hs.251653 tubulin, beta, 2
212907_at	2.75	Consensus includes gb:AI972416 /FEA=EST /DB_XREF=gi:5769332 /DB_XREF=est:wr39d10.x1 /CLONE=IMAGE:2490067 /UG=Hs.24385 Human hbc647 mRNA sequence
209719_x_at	2.75	gb:U19556.1 /DEF=Human squamous cell carcinoma antigen 1 (SCCA1) mRNA, complete cds. /FEA=mRNA /GEN=SCCA1 /PROD=squamous cell carcinoma antigen 1 /DB_XREF=gi:1276435 /UG=Hs.227948 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3 /FL=gb:U19556.1 gb:BC005224.1 gb:NM_006919.1
209953_s_at	2.74	gb:U63131.1 /DEF=Human CDC37 homolog mRNA, complete cds. /FEA=mRNA /PROD=CDC37 homolog /DB_XREF=gi:1421820 /UG=Hs.160958 CDC37 (cell division cycle 37, S. cerevisiae, homolog) /FL=gb:BC000083.1 gb:U43077.1 gb:U63131.1 gb:NM_007065.1
203270_at	2.74	gb:NM_012145.1 /DEF=Homo sapiens deoxythymidylate kinase (thymidylate kinase) (DTYMK), mRNA. /FEA=mRNA /GEN=DTYMK /PROD=deoxythymidylate kinase (thymidylate kinase) /DB_XREF=gi:6912339 /UG=Hs.79006 deoxythymidylate kinase (thymidylate kinase) /FL=gb:BC001827.1 gb:L16991.1 gb:NM_012145.1
219869_s_at	2.74	gb:NM_022154.1 /DEF=Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA. /FEA=mRNA /GEN=LOC64116 /PROD=up-regulated by BCG-CWS /DB_XREF=gi:11545899 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:NM_022154.1
214290_s_at	2.74	Consensus includes gb:AI313324 /FEA=EST /DB_XREF=gi:4018929 /DB_XREF=est:ta77f02.x2

		/CLONE=IMAGE:2050107 /UG=Hs.795 H2A histone family, member O
217785_s_at	2.74	gb:NM_006555.1 /DEF=Homo sapiens SNARE protein (YKT6), mRNA. /FEA=mRNA /GEN=YKT6 /PROD=SNARE protein /DB_XREF=gi:5730119 /UG=Hs.296244 SNARE protein /FL=gb:U95735.1 gb:NM_006555.1
212873_at	2.73	Consensus includes gb:BE349017 /FEA=EST /DB_XREF=gi:9260870 /DB_XREF=est:ht48a03.x1 /CLONE=IMAGE:3149932 /UG=Hs.196914 minor histocompatibility antigen HA-1
202929_s_at	2.72	gb:NM_001355.2 /DEF=Homo sapiens D-dopachrome tautomerase (DDT), mRNA. /FEA=mRNA /GEN=DDT /PROD=D-dopachrome tautomerase /DB_XREF=gi:5453630 /UG=Hs.180015 D-dopachrome tautomerase /FL=gb:U84143.1 gb:U49785.1 gb:NM_001355.2
55093_at	2.72	Cluster Incl. AA534198:nj21a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-993116 /clone_end=3 /gb=AA534198 /gi=2278214 /ug=Hs.86392 /len=603
202736_s_at	2.71	Consensus includes gb:AA112507 /FEA=EST /DB_XREF=gi:1665056 /DB_XREF=est:zm28c01.r1 /CLONE=IMAGE:526944 /UG=Hs.76719 U6 snRNA-associated Sm-like protein /FL=gb:BC000387.1 gb:BC003652.1 gb:AF182290.1 gb:AF117235.1 gb:NM_012321.1 gb:AF251218.1
208977_x_at	2.71	gb:BC004188.1 /DEF=Homo sapiens, tubulin, beta, 2, clone MGC:2826, mRNA, complete cds. /FEA=mRNA /PROD=tubulin, beta, 2 /DB_XREF=gi:13278848 /UG=Hs.251653 tubulin, beta, 2 /FL=gb:BC002783.1 gb:BC002885.1 gb:BC001911.1 gb:BC004188.1 gb:NM_006088.1
210413_x_at	2.71	gb:U19557.1 /DEF=Human squamous cell carcinoma antigen 2 (SCCA2) mRNA, complete cds. /FEA=mRNA /GEN=SCCA2 /PROD=squamous cell carcinoma antigen 2 /DB_XREF=gi:1052870 /UG=Hs.123035 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4 /FL=gb:U19557.1
211003_x_at	2.71	gb:BC003551.1 /DEF=Homo sapiens, Similar to transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase), clone MGC:1193, mRNA, complete cds. /FEA=mRNA /PROD=Similar to transglutaminase 2 (C polypeptide,protein-glutamine-gamma-glutamyltransferase) /DB_XREF=gi:13097680 /UG=Hs.8265 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) /FL=gb:BC003551.1
203729_at	2.7	gb:NM_001425.1 /DEF=Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. /FEA=mRNA /GEN=EMP3 /PROD=epithelial membrane protein 3 /DB_XREF=gi:4503562 /UG=Hs.9999 epithelial membrane protein 3 /FL=gb:U52101.1 gb:U87947.1 gb:NM_001425.1
207390_s_at	2.7	gb:NM_006932.1 /DEF=Homo sapiens smoothelin (SMTN), mRNA. /FEA=mRNA /GEN=SMTN /PROD=smoothelin /DB_XREF=gi:5902099 /UG=Hs.149098 smoothelin /FL=gb:NM_006932.1
208961_s_at	2.7	gb:AB017493.1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger(GBF), complete cds. /FEA=mRNA /PROD=DNA-binding zinc finger(GBF) /DB_XREF=gi:3582142 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM_001300.2
204928_s_at	2.67	gb:NM_019848.2 /DEF=Homo sapiens Protein P3 (P3), mRNA. /FEA=mRNA /GEN=P3 /PROD=Protein P3 /DB_XREF=gi:10938005 /UG=Hs.72980 Protein P3 /FL=gb:NM_019848.2
212233_at	2.67	Consensus includes gb:AL523076 /FEA=EST /DB_XREF=gi:12786569 /DB_XREF=est:AL523076 /CLONE=CS0DC001YI12 (3 prime) /UG=Hs.82503 H.sapiens mRNA for 3UTR of unknown protein
205483_s_at	2.67	gb:NM_005101.1 /DEF=Homo sapiens interferon-stimulated protein, 15 kDa (ISG15), mRNA. /FEA=mRNA /GEN=ISG15 /PROD=interferon-stimulated protein, 15 kDa /DB_XREF=gi:4826773 /UG=Hs.833 interferon-stimulated protein, 15 kDa /FL=gb:M13755.1 gb:NM_005101.1
204451_at	2.67	gb:NM_003505.1 /DEF=Homo sapiens frizzled (Drosophila) homolog 1 (FZD1), mRNA. /FEA=mRNA /GEN=FZD1 /PROD=frizzled 1 /DB_XREF=gi:4503824 /UG=Hs.94234 frizzled (Drosophila) homolog 1 /FL=gb:AB017363.1 gb:NM_003505.1 gb:AF072872.1
209357_at	2.66	gb:AF109161.1 /DEF=Homo sapiens p35srj (MRG1) mRNA, complete cds. /FEA=mRNA /GEN=MRG1 /PROD=p35srj /DB_XREF=gi:4193945 /UG=Hs.82071 Cbpp300-interacting transactivator, with GluAsp-rich

		carboxy-terminal domain, 2 /FL=gb:BC004377.1 gb:AF109161.1
208712_at	2.66	gb:M73554.1 /DEF=Human bcl-1 mRNA, complete CDS. /FEA=mRNA /GEN=bcl-1 /PROD=bcl-1 /DB_XREF=gi:179364 /UG=Hs.82932 cyclin D1 (PRAD1: parathyroid adenomatosis 1) /FL=gb:BC000076.1 gb:M73554.1
213432_at	2.66	Consensus includes gb:AI697108 /FEA=EST /DB_XREF=gi:4985008 /DB_XREF=est:tq14g03.x1 /CLONE=IMAGE:2208820 /UG=Hs.102482 mucin 5, subtype B, tracheobronchial
212782_x_at	2.65	Consensus includes gb:BG335629 /FEA=EST /DB_XREF=gi:13142067 /DB_XREF=est:602404254F1 /CLONE=IMAGE:4542084 /UG=Hs.80475 polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
204221_x_at	2.65	gb:U16307.1 /DEF=Human glioma pathogenesis-related protein (GliPR) mRNA, complete cds. /FEA=mRNA /GEN=GliPR /PROD=glioma pathogenesis-related protein /DB_XREF=gi:1100927 /UG=Hs.64639 glioma pathogenesis-related protein /FL=gb:U16307.1 gb:NM_006851.1
212878_s_at	2.65	Consensus includes gb:AA284075 /FEA=EST /DB_XREF=gi:1928356 /DB_XREF=est:zs49b01.s1 /CLONE=IMAGE:700777 /UG=Hs.117977 kinesin 2 (60-70kD)
208677_s_at	2.64	Consensus includes gb:AL550657 /FEA=EST /DB_XREF=gi:12887837 /DB_XREF=est:AL550657 /CLONE=CS0DI058YI15 (5 prime) /UG=Hs.74631 basigin (OK blood group) /FL=gb:M87879.1 gb:L20471.1 gb:D45131.1 gb:L10240.1 gb:NM_001728.1
202870_s_at	2.63	gb:NM_001255.1 /DEF=Homo sapiens CDC20 (cell division cycle 20, S. cerevisiae, homolog) (CDC20), mRNA. /FEA=mRNA /GEN=CDC20 /PROD=cell division cycle 20 /DB_XREF=gi:4557436 /UG=Hs.82906 CDC20 (cell division cycle 20, S. cerevisiae, homolog) /FL=gb:BC001088.1 gb:AF099644.1 gb:NM_001255.1 gb:U05340.1
209267_s_at	2.63	gb:AB040120.1 /DEF=Homo sapiens mRNA for BCG induced integral membrane protein BIGMo-103, complete cds. /FEA=mRNA /GEN=BIGMo-103 /PROD=BCG induced integral membrane protein BIGMo-103 /DB_XREF=gi:12657580 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:AB040120.1
200783_s_at	2.63	gb:NM_005563.2 /DEF=Homo sapiens leukemia-associated phosphoprotein p18 (stathmin) (LAP18), mRNA. /FEA=mRNA /GEN=LAP18 /PROD=leukemia-associated phosphoprotein p18 /DB_XREF=gi:13518023 /UG=Hs.81915 leukemia-associated phosphoprotein p18 (stathmin) /FL=gb:NM_005563.2 gb:J04991.1
214687_x_at	2.62	Consensus includes gb:AK026577.1 /DEF=Homo sapiens cDNA: FLJ22924 fis, clone KAT06977, highly similar to HSALDAR Human fibroblast mRNA for aldolase A. /FEA=mRNA /DB_XREF=gi:10439461 /UG=Hs.273415 aldolase A, fructose-bisphosphate
201173_x_at	2.62	gb:NM_006600.1 /DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. /FEA=mRNA /GEN=NUDC /PROD=nuclear distribution gene C (A.nidulans)homolog /DB_XREF=gi:5729952 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:BC002399.1 gb:BC003132.1 gb:AB019408.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1
211719_x_at	2.61	gb:BC005858.1 /DEF=Homo sapiens, clone MGC:3255, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:3255) /DB_XREF=gi:13543399 /FL=gb:BC005858.1
221512_at	2.6	gb:AL136683.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D0478 (from clone DKFZp564D0478); complete cds. /FEA=mRNA /GEN=DKFZp564D0478 /PROD=hypothetical protein /DB_XREF=gi:12052889 /UG=Hs.321214 Homo sapiens mRNA; cDNA DKFZp564D0478 (from clone DKFZp564D0478); complete cds /FL=gb:AL136683.1
205083_at	2.6	gb:NM_001159.2 /DEF=Homo sapiens aldehyde oxidase 1 (AOX1), mRNA. /FEA=mRNA /GEN=AOX1 /PROD=aldehyde oxidase 1 /DB_XREF=gi:6598319 /UG=Hs.174151 aldehyde oxidase 1 /FL=gb:AB046692.1 gb:L11005.1 gb:NM_001159.2
213338_at	2.6	Consensus includes gb:BF062629 /FEA=EST /DB_XREF=gi:10821539 /DB_XREF=est:7h62h07.x1 /CLONE=IMAGE:3320605 /UG=Hs.35861 DKFZP586E1621 protein
218115_at	2.59	gb:NM_018154.1 /DEF=Homo sapiens hypothetical protein FLJ10604 (FLJ10604), mRNA. /FEA=mRNA

		/GEN=FLJ10604 /PROD=hypothetical protein FLJ10604 /DB_XREF=gi:8922548 /UG=Hs.26516 hypothetical protein FLJ10604 /FL=gb:NM_018154.1
216041_x_at	2.59	Consensus includes gb:AK023348.1 /DEF=Homo sapiens cDNA FLJ13286 fis, clone OVARC1001154, highly similar to Homo sapiens clone 24720 epithelin 1 and 2 mRNA. /FEA=mRNA /DB_XREF=gi:10435243 /UG=Hs.180577 granulin
201818_at	2.59	gb:NM_024830.1 /DEF=Homo sapiens hypothetical protein FLJ12443 (FLJ12443), mRNA. /FEA=mRNA /GEN=FLJ12443 /PROD=hypothetical protein FLJ12443 /DB_XREF=gi:13376233 /UG=Hs.179882 hypothetical protein FLJ12443 /FL=gb:NM_024830.1
214085_x_at	2.59	Consensus includes gb:AI912583 /FEA=EST /DB_XREF=gi:5632438 /DB_XREF=est:we11d05.x1 /CLONE=IMAGE:2340777 /UG=Hs.154762 HIV-1 rev binding protein 2
202017_at	2.58	gb:NM_000120.2 /DEF=Homo sapiens epoxide hydrolase 1, microsomal (xenobiotic) (EPHX1), mRNA. /FEA=mRNA /GEN=EPHX1 /PROD=epoxide hydrolase 1, microsomal (xenobiotic) /DB_XREF=gi:4557560 /UG=Hs.89649 epoxide hydrolase 1, microsomal (xenobiotic) /FL=gb:BC003567.1 gb:J03518.1 gb:L25878.1 gb:L25879.1 gb:NM_000120.2
202219_at	2.58	gb:NM_005629.1 /DEF=Homo sapiens solute carrier family 6 (neurotransmitter transporter, creatine), member 8 (SLC6A8), mRNA. /FEA=mRNA /GEN=SLC6A8 /PROD=solute carrier family 6 (neurotransmittertransporter, creatine), member 8 /DB_XREF=gi:5032096 /UG=Hs.187958 solute carrier family 6 (neurotransmitter transporter, creatine), member 8 /FL=gb:L31409.1 gb:NM_005629.1
208792_s_at	2.58	gb:M25915.1 /DEF=Human complement cytolysis inhibitor (CLI) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:180619 /UG=Hs.75106 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) /FL=gb:J02908.1 gb:M25915.1 gb:M64722.1 gb:NM_001831.1
204916_at	2.57	gb:NM_005855.1 /DEF=Homo sapiens receptor (calcitonin) activity modifying protein 1 (RAMP1), mRNA. /FEA=mRNA /GEN=RAMP1 /PROD=receptor (calcitonin) activity modifying protein1 precursor /DB_XREF=gi:5032018 /UG=Hs.32989 receptor (calcitonin) activity modifying protein 1 /FL=gb:BC000548.1 gb:NM_005855.1
210869_s_at	2.57	gb:M29277.1 /DEF=Human isolate JuSo MUC18 glycoprotein mRNA (3 variant), complete cds. /FEA=mRNA /PROD=MUC18 glycoprotein /DB_XREF=gi:530047 /UG=Hs.211579 melanoma adhesion molecule /FL=gb:M29277.1
204158_s_at	2.56	gb:NM_006019.1 /DEF=Homo sapiens T-cell, immune regulator 1 (TCIRG1), mRNA. /FEA=mRNA /GEN=TCIRG1 /PROD=ATPase, H+ transporting, 116kD /DB_XREF=gi:5174620 /UG=Hs.46465 T-cell, immune regulator 1 /FL=gb:U45285.1 gb:NM_006019.1
203879_at	2.56	gb:U86453.1 /DEF=Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds. /FEA=mRNA /PROD=phosphatidylinositol 3-kinase catalytic subunitp110delta /DB_XREF=gi:2317893 /UG=Hs.162808 phosphoinositide-3-kinase, catalytic, delta polypeptide /FL=gb:U86453.1 gb:NM_005026.1
209772_s_at	2.55	gb:X69397.1 /DEF=H.sapiens CD24 gene, complete CDS. /FEA=mRNA /GEN=CD24 /PROD=cell surface antigen /DB_XREF=gi:396167 /UG=Hs.286124 CD24 antigen (small cell lung carcinoma cluster 4 antigen) /FL=gb:X69397.1
52078_at	2.55	Cluster Incl. AI828080:wk31e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2413960 /clone_end=3 /gb=AI828080 /gi=5448751 /ug=Hs.4293 /len=544
202391_at	2.55	gb:NM_006317.1 /DEF=Homo sapiens brain acid-soluble protein 1 (BASP1), mRNA. /FEA=mRNA /GEN=BASP1 /PROD=brain acid-soluble protein 1 /DB_XREF=gi:5453749 /UG=Hs.79516 brain abundant, membrane attached signal protein 1 /FL=gb:BC000518.1 gb:AF039656.1 gb:NM_006317.1

203832_at	2.54	gb:NM_003095.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide F (SNRPF), mRNA. /FEA=mRNA /GEN=SNRPF /PROD=small nuclear ribonucleoprotein polypeptide F /DB_XREF=gi:4507130 /UG=Hs.105465 small nuclear ribonucleoprotein polypeptide F /FL=gb:BC002505.1 gb:NM_003095.1
218494_s_at	2.54	gb:NM_020062.1 /DEF=Homo sapiens GLUT4 enhancer factor (GEF), mRNA. /FEA=mRNA /GEN=GEF /PROD=GLUT4 enhancer factor /DB_XREF=gi:13236503 /UG=Hs.170088 GLUT4 enhancer factor /FL=gb:AF249267.3 gb:NM_020062.1
218741_at	2.54	gb:NM_024053.1 /DEF=Homo sapiens hypothetical protein MGC861 (MGC861), mRNA. /FEA=mRNA /GEN=MGC861 /PROD=hypothetical protein MGC861 /DB_XREF=gi:13129021 /UG=Hs.208912 hypothetical protein MGC861 /FL=gb:BC000705.1 gb:NM_024053.1
203968_s_at	2.53	gb:NM_001254.1 /DEF=Homo sapiens CDC6 (cell division cycle 6, S. cerevisiae) homolog (CDC6), mRNA. /FEA=mRNA /GEN=CDC6 /PROD=CDC6 (cell division cycle 6, S. cerevisiae)homolog /DB_XREF=gi:4502702 /UG=Hs.69563 CDC6 (cell division cycle 6, S. cerevisiae) homolog /FL=gb:U77949.1 gb:AF022109.1 gb:NM_001254.1
204331_s_at	2.52	gb:NM_021107.1 /DEF=Homo sapiens mitochondrial ribosomal protein S12 (MRPS12), mRNA. /FEA=mRNA /GEN=MRPS12 /PROD=mitochondrial ribosomal protein S12 /DB_XREF=gi:11056055 /UG=Hs.9964 mitochondrial ribosomal protein S12 /FL=gb:NM_021107.1
203462_x_at	2.51	gb:NM_003751.1 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) (EIF3S9), mRNA. /FEA=mRNA /GEN=EIF3S9 /PROD=eukaryotic translation initiation factor 3,subunit 9 (eta, 116kD) /DB_XREF=gi:4503526 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U62583.1 gb:NM_003751.1
219990_at	2.5	gb:NM_024680.1 /DEF=Homo sapiens hypothetical protein FLJ23311 (FLJ23311), mRNA. /FEA=mRNA /GEN=FLJ23311 /PROD=hypothetical protein FLJ23311 /DB_XREF=gi:13375949 /UG=Hs.94292 hypothetical protein FLJ23311 /FL=gb:NM_024680.1
200916_at	2.5	gb:NM_003564.1 /DEF=Homo sapiens transgelin 2 (TAGLN2), mRNA. /FEA=mRNA /GEN=TAGLN2 /PROD=transgelin 2 /DB_XREF=gi:4507356 /UG=Hs.75725 transgelin 2 /FL=gb:D21261.1 gb:NM_003564.1
32502_at	2.49	Cluster Incl. AL041124:DKFZp434D0316_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434D0316 /clone_end=3 /gb=AL041124 /gi=5410060 /ug=Hs.6748 /len=719
212192_at	2.48	Consensus includes gb:AI718937 /FEA=EST /DB_XREF=gi:5036193 /DB_XREF=est:as50b04.x1 /CLONE=IMAGE:2320591 /UG=Hs.109438 Homo sapiens clone 24775 mRNA sequence
202284_s_at	2.48	gb:NM_000389.1 /DEF=Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), mRNA. /FEA=mRNA /GEN=CDKN1A /PROD=cyclin-dependent kinase inhibitor 1A (p21,Cip1) /DB_XREF=gi:11386202 /UG=Hs.179665 cyclin-dependent kinase inhibitor 1A (p21, Cip1) /FL=gb:NM_000389.1 gb:BC000275.1 gb:BC001935.1 gb:U03106.1 gb:L26165.1 gb:L25610.1 gb:U09579.1
206277_at	2.45	gb:NM_002564.1 /DEF=Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), mRNA. /FEA=mRNA /GEN=P2RY2 /PROD=purinergic receptor P2Y, G-protein coupled, 2 /DB_XREF=gi:4505558 /UG=Hs.339 purinergic receptor P2Y, G-protein coupled, 2 /FL=gb:NM_002564.1 gb:U07225.1
208024_s_at	2.44	gb:NM_005675.1 /DEF=Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA. /FEA=mRNA /GEN=DGCR6 /PROD=DiGeorge syndrome critical region protein 6 /DB_XREF=gi:5031662 /UG=Hs.153910 DiGeorge syndrome critical region gene 6 /FL=gb:AF228707.1 gb:NM_005675.1
208973_at	2.44	gb:BC001072.1 /DEF=Homo sapiens, clone MGC:2683, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:2683) /DB_XREF=gi:12654484 /UG=Hs.151032 hypothetical protein MGC2683 /FL=gb:BC001072.1 gb:BC004456.1
202638_s_at	2.44	gb:NM_000201.1 /DEF=Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus receptor

		(ICAM1), mRNA. /FEA=mRNA /GEN=ICAM1 /PROD=intercellular adhesion molecule 1 precursor /DB_XREF=gi:4557877 /UG=Hs.168383 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor /FL=gb:M24283.1 gb:J03132.1 gb:NM_000201.1
48808_at	2.44	Cluster Incl. AI144299:qb59h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1704443 /clone_end=3 /gb=AI144299 /gi=3666108 /ug=Hs.106843 /len=765
AFFX-r2-Hs18SrRNA-M_x_at	2.44	M10098 Human 18S rRNA sequence, length 1969 bases, middle target bases 647-1292
201950_x_at	2.43	gb:NM_004930.1 /DEF=Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA. /FEA=mRNA /GEN=CAPZB /PROD=F-actin capping protein beta subunit /DB_XREF=gi:4826658 /UG=Hs.76368 capping protein (actin filament) muscle Z-line, beta /FL=gb:NM_004930.1 gb:U03271.1
202619_s_at	2.43	Consensus includes gb:AI754404 /FEA=EST /DB_XREF=gi:5132668 /DB_XREF=est:cr24g06.x1 /CLONE=HBMSC_cr24g06 /UG=Hs.41270 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 /FL=gb:U84573.1 gb:NM_000935.1
201466_s_at	2.42	gb:NM_002228.2 /DEF=Homo sapiens v-jun avian sarcoma virus 17 oncogene homolog (JUN), mRNA. /FEA=mRNA /GEN=JUN /PROD=v-jun avian sarcoma virus 17 oncogene homolog /DB_XREF=gi:7710122 /UG=Hs.78465 v-jun avian sarcoma virus 17 oncogene homolog /FL=gb:BC002646.1 gb:NM_002228.2
213476_x_at	2.42	Consensus includes gb:AL565749 /FEA=EST /DB_XREF=gi:12917434 /DB_XREF=est:AL565749 /CLONE=CS0DF007YJ03 (3 prime) /UG=Hs.159154 tubulin, beta, 4
204728_s_at	2.42	gb:NM_007086.1 /DEF=Homo sapiens AND-1 protein (AND-1), mRNA. /FEA=mRNA /GEN=AND-1 /PROD=AND-1 protein /DB_XREF=gi:5901891 /UG=Hs.72160 AND-1 protein /FL=gb:NM_007086.1
209482_at	2.4	gb:BC001430.1 /DEF=Homo sapiens, POP7 (processing of precursor, S. cerevisiae) homolog, clone MGC:1986, mRNA, complete cds. /FEA=mRNA /PROD=POP7 (processing of precursor, S. cerevisiae)homolog /DB_XREF=gi:12655150 /UG=Hs.18747 POP7 (processing of precursor, S. cerevisiae) homolog /FL=gb:BC001430.1 gb:U94316.1 gb:NM_005837.1
200736_s_at	2.4	gb:NM_000581.1 /DEF=Homo sapiens glutathione peroxidase 1 (GPX1), mRNA. /FEA=mRNA /GEN=GPX1 /PROD=glutathione peroxidase 1 /DB_XREF=gi:10834975 /UG=Hs.76686 glutathione peroxidase 1 /FL=gb:NM_000581.1 gb:BC000742.1 gb:M21304.1
200966_x_at	2.4	gb:NM_000034.1 /DEF=Homo sapiens aldolase A, fructose-bisphosphate (ALDOA), mRNA. /FEA=mRNA /GEN=ALDOA /PROD=aldolase A /DB_XREF=gi:4557304 /UG=Hs.273415 aldolase A, fructose-bisphosphate /FL=gb:BC004333.1 gb:M11560.1 gb:NM_000034.1
AFFX-M27830_M_at	2.4	M27830 Human 28S ribosomal RNA gene, complete cds (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
212567_s_at	2.4	Consensus includes gb:AL523310 /FEA=EST /DB_XREF=gi:12786803 /DB_XREF=est:AL523310 /CLONE=CS0DC001YN06 (3 prime) /UG=Hs.150580 putative translation initiation factor
212212_s_at	2.39	Consensus includes gb:BF055496 /FEA=EST /DB_XREF=gi:10809392 /DB_XREF=est:7j80h12.x1 /CLONE=IMAGE:3392807 /UG=Hs.112184 DKFZP586J0619 protein
217294_s_at	2.39	Consensus includes gb:U88968.1 /DEF=Human alpha enolase like 1 (ENO1L1) mRNA, partial cds. /FEA=mRNA /GEN=ENO1L1 /PROD=alpha enolase like 1 /DB_XREF=gi:3282242 /UG=Hs.254105 enolase 1, (alpha)
218034_at	2.39	gb:NM_016068.1 /DEF=Homo sapiens CGI-135 protein (LOC51024), mRNA. /FEA=mRNA /GEN=LOC51024 /PROD=CGI-135 protein /DB_XREF=gi:7705631 /UG=Hs.84344 CGI-135 protein /FL=gb:BC003540.1 gb:AF151893.1 gb:NM_016068.1
211924_s_at	2.39	gb:AY029180.1 /DEF=Homo sapiens soluble urokinase plasminogen activator receptor precursor (SUPAR) mRNA,

		complete cds. /FEA=CDS /GEN=SUPAR /PROD=soluble urokinase plasminogen activator receptorprecursor /DB_XREF=gi:13641308 /FL=gb:AY029180.1
201555_at	2.38	gb:NM_002388.2 /DEF=Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA. /FEA=mRNA /GEN=MCM3 /PROD=minichromosome maintenance deficient (S.cerevisiae) 3 /DB_XREF=gi:6631094 /UG=Hs.179565 minichromosome maintenance deficient (S. cerevisiae) 3 /FL=gb:BC001626.1 gb:NM_002388.2 gb:D38073.1
205516_x_at	2.38	gb:NM_012127.1 /DEF=Homo sapiens Cip1-interacting zinc finger protein (CIZ1), mRNA. /FEA=mRNA /GEN=CIZ1 /PROD=Cip1-interacting zinc finger protein /DB_XREF=gi:6912307 /UG=Hs.23476 Cip1-interacting zinc finger protein /FL=gb:AB030835.1 gb:AF159025.1 gb:NM_012127.1
203411_s_at	2.38	gb:NM_005572.1 /DEF=Homo sapiens lamin AC (LMNA), mRNA. /FEA=mRNA /GEN=LMNA /PROD=lamin AC /DB_XREF=gi:5031874 /UG=Hs.77886 lamin AC /FL=gb:BC000511.1 gb:BC003162.1 gb:M13451.1 gb:NM_005572.1
202580_x_at	2.37	gb:NM_021953.1 /DEF=Homo sapiens forkhead box M1 (FOXM1), mRNA. /FEA=mRNA /GEN=FOXM1 /PROD=forkhead box M1 /DB_XREF=gi:11386144 /UG=Hs.239 forkhead box M1 /FL=gb:NM_021953.1 gb:U83113.1 gb:L16783.1
218493_at	2.37	gb:NM_024571.1 /DEF=Homo sapiens hypothetical protein FLJ22940 (FLJ22940), mRNA. /FEA=mRNA /GEN=FLJ22940 /PROD=hypothetical protein FLJ22940 /DB_XREF=gi:13443017 /UG=Hs.15277 hypothetical protein FLJ22940 /FL=gb:BC001381.1 gb:NM_024571.1
AFFX-M27830_5_at	2.37	M27830 Human 28S ribosomal RNA gene, complete cds (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
210845_s_at	2.37	gb:U08839.1 /DEF=Human urokinase-type plasminogen activator receptor mRNA, complete cds. /FEA=mRNA /PROD=urokinase-type plasminogen activator receptor /DB_XREF=gi:517197 /UG=Hs.179657 plasminogen activator, urokinase receptor /FL=gb:U08839.1
205462_s_at	2.37	gb:NM_002149.1 /DEF=Homo sapiens hippocalcin-like 1 (HPCAL1), mRNA. /FEA=mRNA /GEN=HPCAL1 /PROD=hippocalcin-like 1 /DB_XREF=gi:4504474 /UG=Hs.3618 hippocalcin-like 1 /FL=gb:NM_002149.1 gb:D16227.1
213629_x_at	2.37	Consensus includes gb:BF246115 /FEA=EST /DB_XREF=gi:11160133 /DB_XREF=est:601854068F1 /CLONE=IMAGE:4073921 /UG=Hs.8765 RNA helicase-related protein
201082_s_at	2.36	gb:NM_004082.2 /DEF=Homo sapiens dynactin 1 (p150, Glued (Drosophila) homolog) (DCTN1), transcript variant 1, mRNA. /FEA=mRNA /GEN=DCTN1 /PROD=dynactin 1, isoform 1 /DB_XREF=gi:13259509 /UG=Hs.74617 dynactin 1 (p150, Glued (Drosophila) homolog) /FL=gb:NM_023019.1 gb:NM_004082.2
218060_s_at	2.36	gb:NM_024598.1 /DEF=Homo sapiens hypothetical protein FLJ13154 (FLJ13154), mRNA. /FEA=mRNA /GEN=FLJ13154 /PROD=hypothetical protein FLJ13154 /DB_XREF=gi:13375796 /UG=Hs.25303 hypothetical protein FLJ13154 /FL=gb:BC004415.1 gb:NM_024598.1
50314_i_at	2.36	Cluster Incl. AI761506:wi61b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394717 /clone_end=3 /gb=AI761506 /gi=5177173 /ug=Hs.239692 /len=544
202718_at	2.36	gb:NM_000597.1 /DEF=Homo sapiens insulin-like growth factor binding protein 2 (36kD) (IGFBP2), mRNA. /FEA=mRNA /GEN=IGFBP2 /PROD=insulin-like growth factor binding protein 2(36kD) /DB_XREF=gi:10835156 /UG=Hs.162 insulin-like growth factor binding protein 2 (36kD) /FL=gb:NM_000597.1 gb:BC004312.1 gb:M35410.1
201954_at	2.36	gb:NM_005720.1 /DEF=Homo sapiens actin related protein 23 complex, subunit 1A (41 kD) (ARPC1B), mRNA. /FEA=mRNA /GEN=ARPC1B /PROD=actin related protein 23 complex, subunit 1A(41 kD) /DB_XREF=gi:5031600 /UG=Hs.11538 actin related protein 23 complex, subunit 1A (41 kD) /FL=gb:BC002562.1 gb:AF006084.1 gb:NM_005720.1

217992_s_at	2.36	gb:NM_024329.1 /DEF=Homo sapiens hypothetical protein MGC4342 (MGC4342), mRNA. /FEA=mRNA /GEN=MGC4342 /PROD=hypothetical protein MGC4342 /DB_XREF=gi:13443015 /UG=Hs.301342 hypothetical protein MGC4342 /FL=gb:BC003033.1 gb:NM_024329.1
202510_s_at	2.36	gb:NM_006291.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA. /FEA=mRNA /GEN=TNFAIP2 /PROD=tumor necrosis factor, alpha-induced protein 2 /DB_XREF=gi:5454133 /UG=Hs.101382 tumor necrosis factor, alpha-induced protein 2 /FL=gb:M92357.1 gb:NM_006291.1
209440_at	2.35	gb:BC001605.1 /DEF=Homo sapiens, phosphoribosyl pyrophosphate synthetase 1, clone MGC:2256, mRNA, complete cds. /FEA=mRNA /PROD=phosphoribosyl pyrophosphate synthetase 1 /DB_XREF=gi:12804406 /UG=Hs.56 phosphoribosyl pyrophosphate synthetase 1 /FL=gb:BC001605.1 gb:D00860.1
210524_x_at	2.35	gb:AF078844.1 /DEF=Homo sapiens hqp0376 protein mRNA, complete cds. /FEA=mRNA /PROD=hqp0376 protein /DB_XREF=gi:6683748 /UG=Hs.8765 RNA helicase-related protein /FL=gb:AF078844.1
203434_s_at	2.34	Consensus includes gb:AI433463 /FEA=EST /DB_XREF=gi:4289355 /DB_XREF=est:ti65g11.x1 /CLONE=IMAGE:2136932 /UG=Hs.1298 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) /FL=gb:J03779.1 gb:NM_007287.1 gb:NM_007288.1
206569_at	2.34	gb:NM_006850.1 /DEF=Homo sapiens suppression of tumorigenicity 16 (melanoma differentiation) (ST16), mRNA. /FEA=mRNA /GEN=ST16 /PROD=suppression of tumorigenicity 16 (melanomadifferentiation) /DB_XREF=gi:5803085 /UG=Hs.315463 suppression of tumorigenicity 16 (melanoma differentiation) /FL=gb:U16261.1 gb:NM_006850.1
209156_s_at	2.34	gb:AY029208.1 /DEF=Homo sapiens type VI collagen alpha 2 chain precursor (COL6A2) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=COL6A2 /PROD=type VI collagen alpha 2 chain precursor /DB_XREF=gi:13603393 /UG=Hs.159263 collagen, type VI, alpha 2 /FL=gb:AY029208.1
216606_x_at	2.33	Consensus includes gb:AL050332 /DEF=Human DNA sequence from clone RP4-570F3 on chromosome 6 Contains a gene similar to Rattus norvegicus synaptic ras GTPase-activating protein p135, the CICK0721Q.5 (polypeptide from patented cDNA Em:E06811) gene, the PHF1 (PHD finger protein 1) gen... /FEA=mRNA_1 /DB_XREF=gi:6010176 /UG=Hs.306238 acyl-protein
207850_at	2.33	gb:NM_002090.1 /DEF=Homo sapiens GRO3 oncogene (GRO3), mRNA. /FEA=mRNA /GEN=GRO3 /PROD=GRO3 oncogene /DB_XREF=gi:4504156 /UG=Hs.89690 GRO3 oncogene /FL=gb:M36821.1 gb:NM_002090.1
218154_at	2.33	gb:NM_024736.1 /DEF=Homo sapiens hypothetical protein FLJ12150 (FLJ12150), mRNA. /FEA=mRNA /GEN=FLJ12150 /PROD=hypothetical protein FLJ12150 /DB_XREF=gi:13376057 /UG=Hs.118983 hypothetical protein FLJ12150 /FL=gb:NM_024736.1
202757_at	2.33	gb:NM_015456.1 /DEF=Homo sapiens DKFZP586B0519 protein (DKFZP586B0519), mRNA. /FEA=mRNA /GEN=DKFZP586B0519 /PROD=DKFZP586B0519 protein /DB_XREF=gi:7661663 /UG=Hs.27633 DKFZP586B0519 protein /FL=gb:AL050280.1 gb:NM_015456.1
201618_x_at	2.33	gb:NM_003801.2 /DEF=Homo sapiens anchor attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. /FEA=mRNA /GEN=GPAA1 /PROD=anchor attachment protein 1 /DB_XREF=gi:6031166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2
209318_x_at	2.33	Consensus includes gb:BG547855 /FEA=EST /DB_XREF=gi:13546520 /DB_XREF=est:602576153F1 /CLONE=IMAGE:4704108 /UG=Hs.75825 pleiomorphic adenoma gene-like 1 /FL=gb:U72621.3
209715_at	2.32	gb:L07515.1 /DEF=Human heterochromatin protein homologue (HP1) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:184310 /UG=Hs.89232 chromobox homolog 5 (Drosophila HP1 alpha) /FL=gb:L07515.1 gb:NM_012117.1

212464_s_at	2.32	Consensus includes gb:X02761.1 /DEF=Human mRNA for fibronectin (FN precursor). /FEA=mRNA /PROD=fibronectin precursor /DB_XREF=gi:31396 /UG=Hs.287820 fibronectin 1
201369_s_at	2.32	gb:NM_006887.1 /DEF=Homo sapiens butyrate response factor 2 (EGF-response factor 2) (BRF2), mRNA. /FEA=mRNA /GEN=BRF2 /PROD=butyrate response factor 2 (EGF-response factor2) /DB_XREF=gi:5901899 /UG=Hs.78909 butyrate response factor 2 (EGF-response factor 2) /FL=gb:BC005010.1 gb:NM_006887.1
209708_at	2.31	gb:AY007239.1 /DEF=Homo sapiens monooxygenase X mRNA, complete cds. /FEA=mRNA /PROD=monooxygenase X /DB_XREF=gi:9988949 /UG=Hs.6909 DKFZP564G202 protein /FL=gb:AY007239.1
218280_x_at	2.31	gb:NM_003516.1 /DEF=Homo sapiens H2A histone family, member O (H2AFO), mRNA. /FEA=mRNA /GEN=H2AFO /PROD=H2A histone family, member O /DB_XREF=gi:4504250 /UG=Hs.795 H2A histone family, member O /FL=gb:BC001629.1 gb:L19779.1 gb:NM_003516.1
205364_at	2.31	gb:NM_003500.1 /DEF=Homo sapiens acyl-Coenzyme A oxidase 2, branched chain (ACOX2), mRNA. /FEA=mRNA /GEN=ACOX2 /PROD=acyl-Coenzyme A oxidase 2, branched chain /DB_XREF=gi:4501868 /UG=Hs.9795 acyl-Coenzyme A oxidase 2, branched chain /FL=gb:NM_003500.1
212082_s_at	2.31	Consensus includes gb:BE734356 /FEA=EST /DB_XREF=gi:10148348 /DB_XREF=est:601565603F1 /CLONE=IMAGE:3840385 /UG=Hs.77385 myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
208625_s_at	2.31	gb:AF104913.1 /DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic protein synthesis initiation factor /DB_XREF=gi:3941723 /UG=Hs.211568 eukaryotic translation initiation factor 4 gamma, 1 /FL=gb:AF104913.1
211573_x_at	2.31	gb:M98478.1 /DEF=Human transglutaminase mRNA, complete cds. /FEA=mRNA /PROD=transglutaminase /DB_XREF=gi:339577 /UG=Hs.8265 transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) /FL=gb:M98478.1
218681_s_at	2.31	gb:NM_022044.1 /DEF=Homo sapiens stromal cell-derived factor 2-like 1 (SDF2L1), mRNA. /FEA=mRNA /GEN=SDF2L1 /PROD=stromal cell-derived factor 2-like 1 /DB_XREF=gi:11545742 /UG=Hs.303116 stromal cell-derived factor 2-like 1 /FL=gb:AB043007.1 gb:NM_022044.1
204559_s_at	2.3	gb:NM_016199.1 /DEF=Homo sapiens U6 snRNA-associated Sm-like protein LSm7 (LOC51690), mRNA. /FEA=mRNA /GEN=LOC51690 /PROD=U6 snRNA-associated Sm-like protein LSm7 /DB_XREF=gi:7706422 /UG=Hs.70830 U6 snRNA-associated Sm-like protein LSm7 /FL=gb:AF182293.1 gb:NM_016199.1
37012_at	2.3	Cluster Incl. U03271:Human F-actin capping protein beta subunit mRNA, complete cds /cds=(0,818) /gb=U03271 /gi=595256 /ug=Hs.76368 /len=1077
220189_s_at	2.3	gb:NM_014275.1 /DEF=Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B (MGAT4B), mRNA. /FEA=mRNA /GEN=MGAT4B /PROD=mannosyl (alpha-1,3-)-glycoproteinbeta-1,4-N-acetylglucosaminyltransferase, isoenzyme B /DB_XREF=gi:7710151 /UG=Hs.4867 mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B /FL=gb:AB000624.1 gb:NM_014275.1
209263_x_at	2.29	gb:BC000389.1 /DEF=Homo sapiens, transmembrane 4 superfamily member 7, clone MGC:8437, mRNA, complete cds. /FEA=mRNA /PROD=transmembrane 4 superfamily member 7 /DB_XREF=gi:12653240 /UG=Hs.26518 transmembrane 4 superfamily member 7 /FL=gb:BC000389.1 gb:AF022813.1 gb:AF054841.1 gb:NM_003271.1
200078_s_at	2.29	gb:BC005876.1 /DEF=Homo sapiens, ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD, clone MGC:4498, mRNA, complete cds. /FEA=mRNA /PROD=ATPase, H+ transporting, lysosomal (vacuolarproton pump) 21kD /DB_XREF=gi:13543437 /FL=gb:BC005876.1
203300_x_at	2.29	gb:NM_003916.1 /DEF=Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA. /FEA=mRNA /GEN=AP1S2 /PROD=adaptor-related protein complex 1, sigma 2subunit /DB_XREF=gi:4506956

		/UG=Hs.40368 adaptor-related protein complex 1, sigma 2 subunit /FL=gb:AF251295.1 gb:BC001117.1 gb:AB015320.1 gb:NM_003916.1
220734_s_at	2.28	gb:NM_030575.1 /DEF=Homo sapiens hypothetical protein MGC10334 (MGC10334), mRNA. /FEA=mRNA /GEN=MGC10334 /PROD=hypothetical protein MGC10334 /DB_XREF=gi:13386487 /UG=Hs.302446 hypothetical protein MGC10334 /FL=gb:BC004366.1 gb:NM_030575.1
201185_at	2.28	gb:NM_002775.1 /DEF=Homo sapiens protease, serine, 11 (IGF binding) (PRSS11), mRNA. /FEA=mRNA /GEN=PRSS11 /PROD=protease, serine, 11 (IGF binding) /DB_XREF=gi:4506140 /UG=Hs.75111 protease, serine, 11 (IGF binding) /FL=gb:D87258.1 gb:NM_002775.1
201393_s_at	2.28	gb:NM_000876.1 /DEF=Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA. /FEA=mRNA /GEN=IGF2R /PROD=insulin-like growth factor 2 receptor /DB_XREF=gi:4504610 /UG=Hs.76473 insulin-like growth factor 2 receptor /FL=gb:J03528.1 gb:NM_000876.1
202669_s_at	2.27	gb:U16797.1 /DEF=Human LERK-5 (EPLG5) mRNA, complete cds. /FEA=mRNA /GEN=EPLG5 /PROD=LERK-5 /DB_XREF=gi:902370 /UG=Hs.30942 ephrin-B2 /FL=gb:U81262.1 gb:NM_004093.1 gb:L38734.1 gb:U16797.1
AFFX-HSAC07/X00351_5_at	2.27	X00351 Human mRNA for beta-actin (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
202206_at	2.27	Consensus includes gb:AW450363 /FEA=EST /DB_XREF=gi:6991139 /DB_XREF=est:UI-H-BI3-akn-d-02-0-UI.s1 /CLONE=IMAGE:2734875 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
200632_s_at	2.26	gb:NM_006096.1 /DEF=Homo sapiens N-myc downstream regulated (NDRG1), mRNA. /FEA=mRNA /GEN=NDRG1 /PROD=N-myc downstream regulated /DB_XREF=gi:5174656 /UG=Hs.75789 N-myc downstream regulated /FL=gb:BC003175.1 gb:D87953.1 gb:AF004162.1 gb:NM_006096.1
217766_s_at	2.26	gb:NM_014313.1 /DEF=Homo sapiens small membrane protein 1 (SMP1), mRNA. /FEA=mRNA /GEN=SMP1 /PROD=small membrane protein 1 /DB_XREF=gi:7657594 /UG=Hs.107979 small membrane protein 1 /FL=gb:AL136627.1 gb:AF081282.1 gb:NM_014313.1
204175_at	2.25	gb:NM_015871.1 /DEF=Homo sapiens zinc finger protein (LOC51042), mRNA. /FEA=mRNA /GEN=LOC51042 /PROD=zinc finger protein /DB_XREF=gi:7705661 /UG=Hs.102419 zinc finger protein /FL=gb:BC002580.1 gb:D45213.1 gb:NM_015871.1
207172_s_at	2.25	gb:NM_001797.1 /DEF=Homo sapiens cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), mRNA. /FEA=mRNA /GEN=CDH11 /PROD=cadherin 11, type 2, OB-cadherin (osteoblast) /DB_XREF=gi:4502716 /UG=Hs.75929 cadherin 11, type 2, OB-cadherin (osteoblast) /FL=gb:NM_001797.1 gb:L34056.1 gb:D21254.1
212647_at	2.24	Consensus includes gb:NM_006270.1 /DEF=Homo sapiens related RAS viral (r-ras) oncogene homolog (RRAS), mRNA. /FEA=CDS /GEN=RRAS /PROD=related RAS viral (r-ras) oncogene homolog /DB_XREF=gi:5454027 /UG=Hs.9651 related RAS viral (r-ras) oncogene homolog /FL=gb:NM_006270.1
215101_s_at	2.24	Consensus includes gb:BG166705 /FEA=EST /DB_XREF=gi:12673408 /DB_XREF=est:602339217F1 /CLONE=IMAGE:4447013 /UG=Hs.89714 small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78)
200787_s_at	2.24	gb:BC002426.1 /DEF=Homo sapiens, phosphoprotein enriched in astrocytes 15, clone MGC:1685, mRNA, complete cds. /FEA=mRNA /PROD=phosphoprotein enriched in astrocytes 15 /DB_XREF=gi:12803230 /UG=Hs.194673 phosphoprotein enriched in astrocytes 15 /FL=gb:BC002426.1 gb:NM_003768.1
201109_s_at	2.23	Consensus includes gb:AV726673 /FEA=EST /DB_XREF=gi:10836094 /DB_XREF=est:AV726673 /CLONE=HTCBGC12 /UG=Hs.87409 thrombospondin 1 /FL=gb:NM_003246.1
201245_s_at	2.23	Consensus includes gb:AL523776 /FEA=EST /DB_XREF=gi:12787269 /DB_XREF=est:AL523776

		/CLONE=CS0DC003YC23 (5 prime) /UG=Hs.108504 hypothetical protein FLJ20113 /FL=gb:NM_017670.1
205743_at	2.23	gb:NM_003149.1 /DEF=Homo sapiens src homology three (SH3) and cysteine rich domain (STAC), mRNA. /FEA=mRNA /GEN=STAC /PROD=src homology three (SH3) and cysteine richdomain /DB_XREF=gi:4507246 /UG=Hs.56045 src homology three (SH3) and cysteine rich domain /FL=gb:D86640.1 gb:NM_003149.1
208688_x_at	2.23	gb:U78525.1 /DEF=Homo sapiens eukaryotic translation initiation factor (eIF3) mRNA, complete cds. /FEA=mRNA /GEN=eIF3 /PROD=eukaryotic translation initiation factor /DB_XREF=gi:2558667 /UG=Hs.57783 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) /FL=gb:U78525.1
221263_s_at	2.23	gb:NM_031287.1 /DEF=Homo sapiens hypothetical protein MGC3133 (MGC3133), mRNA. /FEA=mRNA /GEN=MGC3133 /PROD=hypothetical protein MGC3133 /DB_XREF=gi:13775199 /FL=gb:NM_031287.1
200885_at	2.22	gb:NM_005167.1 /DEF=Homo sapiens ras homolog gene family, member C (ARHC), mRNA. /FEA=mRNA /GEN=ARHC /PROD=ras homolog gene family, member C /DB_XREF=gi:4885066 /UG=Hs.179735 ras homolog gene family, member C /FL=gb:L25081.1 gb:NM_005167.1
36936_at	2.22	Cluster Incl. U58766:Human FX protein mRNA, complete cds /cds=(74,1039) /gb=U58766 /gi=1381178 /ug=Hs.75801 /len=1330
218636_s_at	2.22	gb:NM_016219.1 /DEF=Homo sapiens alpha 1,2-mannosidase (LOC51697), mRNA. /FEA=mRNA /GEN=LOC51697 /PROD=alpha 1,2-mannosidase /DB_XREF=gi:7706436 /UG=Hs.279881 alpha 1,2-mannosidase /FL=gb:BC002953.1 gb:AF148509.1 gb:NM_016219.1
202123_s_at	2.22	gb:NM_005157.2 /DEF=Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 1 (ABL1), transcript variant a, mRNA. /FEA=mRNA /GEN=ABL1 /PROD=v-abl Abelson murine leukemia viral oncogenehomolog 1 isoform a /DB_XREF=gi:6382056 /UG=Hs.146355 v-abl Abelson murine leukemia viral oncogene homolog 1 /FL=gb:M14752.1 gb:NM_005157.2
202587_s_at	2.22	gb:BC001116.1 /DEF=Homo sapiens, adenylate kinase 1, clone MGC:1808, mRNA, complete cds. /FEA=mRNA /PROD=adenylate kinase 1 /DB_XREF=gi:12654562 /UG=Hs.76240 adenylate kinase 1 /FL=gb:BC001116.1 gb:NM_000476.1 gb:AB021871.1
212430_at	2.22	Consensus includes gb:AL109955 /DEF=Human DNA sequence from clone RP4-800J21 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the 3 part of the RAE1 gene for a homolog to RNA export protein 1 from S.pombe and the gene for the ssDNA binding protein SEB4D.n /FEA=mRNA_1 /DB_XREF=gi:11558768 /UG=Hs.236361 seb4D
212016_s_at	2.21	Consensus includes gb:AA679988 /FEA=EST /DB_XREF=gi:2656455 /DB_XREF=est:ag51f11.s1 /CLONE=IMAGE:1126509 /UG=Hs.172550 polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I)
218188_s_at	2.21	gb:NM_012458.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 13 (yeast) homolog B (TIMM13B), mRNA. /FEA=mRNA /GEN=TIMM13B /PROD=translocase of inner mitochondrial membrane 13(yeast) homolog B /DB_XREF=gi:11024699 /UG=Hs.23410 translocase of inner mitochondrial membrane 13 (yeast) homolog B /FL=gb:NM_012458.1 gb:AF144700.1 gb:AF152352.1
203054_s_at	2.21	gb:NM_022171.1 /DEF=Homo sapiens T-cell leukemia translocation altered gene (TCTA), mRNA. /FEA=mRNA /GEN=TCTA /PROD=T-cell leukemia translocation altered gene /DB_XREF=gi:11560140 /UG=Hs.250894 T-cell leukemia translocation altered gene /FL=gb:NM_022171.1 gb:BC005157.1
216841_s_at	2.21	Consensus includes gb:X15132.1 /DEF=Human mRNA for manganese containing superoxide dismutase (EC 1.15.1.1). /FEA=mRNA /DB_XREF=gi:34794 /UG=Hs.318885 superoxide dismutase 2, mitochondrial
205498_at	2.2	gb:NM_000163.1 /DEF=Homo sapiens growth hormone receptor (GHR), mRNA. /FEA=mRNA /GEN=GHR /PROD=growth hormone receptor /DB_XREF=gi:4503992 /UG=Hs.125180 growth hormone receptor /FL=gb:NM_000163.1

201578_at	2.2	gb:NM_005397.1 /DEF=Homo sapiens podocalyxin-like (PODXL), mRNA. /FEA=mRNA /GEN=PODXL /PROD=podocalyxin-like /DB_XREF=gi:4885556 /UG=Hs.16426 podocalyxin-like /FL=gb:U97519.1 gb:NM_005397.1
203767_s_at	2.2	Consensus includes gb:AI122754 /FEA=EST /DB_XREF=gi:3538520 /DB_XREF=est:qa48e01.x1 /CLONE=IMAGE:1690008 /UG=Hs.79876 steroid sulfatase (microsomal), arylsulfatase C, isozyme S /FL=gb:NM_000351.2 gb:M16505.1 gb:J04964.1
211060_x_at	2.19	gb:BC006383.1 /DEF=Homo sapiens, clone MGC:12663, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:12663) /DB_XREF=gi:13623546 /FL=gb:BC006383.1
201541_s_at	2.19	gb:NM_006349.1 /DEF=Homo sapiens putative cyclin G1 interacting protein (CG1I), mRNA. /FEA=mRNA /GEN=CG1I /PROD=putative cyclin G1 interacting protein /DB_XREF=gi:5453616 /UG=Hs.10028 putative cyclin G1 interacting protein /FL=gb:U61837.1 gb:NM_006349.1
201168_x_at	2.19	gb:NM_004309.1 /DEF=Homo sapiens Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA), mRNA. /FEA=mRNA /GEN=ARHGDIA /PROD=Rho GDP dissociation inhibitor (GDI) alpha /DB_XREF=gi:4757767 /UG=Hs.159161 Rho GDP dissociation inhibitor (GDI) alpha /FL=gb:D13989.1 gb:M97579.1 gb:NM_004309.1
219500_at	2.19	gb:NM_013246.1 /DEF=Homo sapiens cardiotrophin-like cytokine; neurotrophin-1B-cell stimulating factor-3 (CLC), mRNA. /FEA=mRNA /GEN=CLC /PROD=cardiotrophin-like cytokine;neurotrophin-1B-cell stimulating factor-3 /DB_XREF=gi:7019350 /UG=Hs.132004 cardiotrophin-like cytokine; neurotrophin-1B-cell stimulating factor-3 /FL=gb:AF172854.1 gb:AF176911.1 gb:NM_013246.1
211358_s_at	2.18	gb:AF234161.1 /DEF=Homo sapiens nuclear protein NP94b (NP94) mRNA, complete cds, alternatively spliced. /FEA=mRNA /GEN=NP94 /PROD=nuclear protein NP94b /DB_XREF=gi:7188807 /UG=Hs.23476 Cip1-interacting zinc finger protein /FL=gb:AF234161.1
202424_at	2.17	gb:NM_030662.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 2 (MAP2K2), mRNA. /FEA=mRNA /GEN=MAP2K2 /PROD=mitogen-activated protein kinase kinase 2 /DB_XREF=gi:13489053 /UG=Hs.72241 mitogen-activated protein kinase kinase 2 /FL=gb:BC000471.1 gb:NM_030662.1
218770_s_at	2.17	gb:NM_018056.1 /DEF=Homo sapiens hypothetical protein FLJ10315 (FLJ10315), mRNA. /FEA=mRNA /GEN=FLJ10315 /PROD=hypothetical protein FLJ10315 /DB_XREF=gi:8922347 /UG=Hs.25544 hypothetical protein FLJ10315 /FL=gb:AL136695.1 gb:NM_018056.1
211284_s_at	2.17	gb:BC000324.1 /DEF=Homo sapiens, Similar to granulin, clone MGC:8480, mRNA, complete cds. /FEA=mRNA /PROD=Similar to granulin /DB_XREF=gi:12653114 /UG=Hs.180577 granulin /FL=gb:BC000324.1
202096_s_at	2.16	gb:NM_000714.2 /DEF=Homo sapiens benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA. /FEA=mRNA /GEN=BZRP /PROD=peripheral benzodiazapine receptor /DB_XREF=gi:6382068 /UG=Hs.202 benzodiazapine receptor (peripheral) /FL=gb:BC001110.1 gb:M36035.1 gb:NM_000714.2
217949_s_at	2.16	gb:NM_024006.1 /DEF=Homo sapiens hypothetical protein IMAGE3455200 (IMAGE3455200), mRNA. /FEA=mRNA /GEN=IMAGE3455200 /PROD=hypothetical protein IMAGE3455200 /DB_XREF=gi:13124769 /UG=Hs.324844 hypothetical protein IMAGE3455200 /FL=gb:BC002911.1 gb:NM_024006.1
201115_at	2.16	gb:NM_006230.1 /DEF=Homo sapiens polymerase (DNA directed), delta 2, regulatory subunit (50kD) (POLD2), mRNA. /FEA=mRNA /GEN=POLD2 /PROD=polymerase (DNA directed), delta 2, regulatorysubunit (50kD) /DB_XREF=gi:5453923 /UG=Hs.74598 polymerase (DNA directed), delta 2, regulatory subunit (50kD) /FL=gb:U21090.1 gb:BC000459.1 gb:NM_006230.1
210428_s_at	2.16	gb:AF260566.1 /DEF=Homo sapiens hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (HRS) mRNA, complete cds. /FEA=mRNA /GEN=HRS /PROD=hepatocyte growth factor-regulated tyrosinekinase substrate HRS isoform 2 /DB_XREF=gi:9022388 /UG=Hs.24756 hepatocyte growth factor-regulated tyrosine

		kinase substrate /FL=gb:AF260566.1
202888_s_at	2.16	gb:NM_001150.1 /DEF=Homo sapiens alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA. /FEA=mRNA /GEN=ANPEP /PROD=membrane alanine aminopeptidase precursor /DB_XREF=gi:4502094 /UG=Hs.1239 alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) /FL=gb:M22324.1 gb:NM_001150.1
209821_at	2.15	gb:AB024518.1 /DEF=Homo sapiens mRNA for DVS27-related protein, complete cds. /FEA=mRNA /GEN=DVS27 /PROD=DVS27-related protein /DB_XREF=gi:4520327 /UG=Hs.58589 glycogenin 2 /FL=gb:AB024518.1
210042_s_at	2.15	gb:AF073890.1 /DEF=Homo sapiens cathepsin X precursor, mRNA, complete cds. /FEA=mRNA /PROD=cathepsin X precursor /DB_XREF=gi:3650497 /UG=Hs.252549 cathepsin Z /FL=gb:AF032906.1 gb:AF073890.1 gb:NM_001336.1 gb:AF136273.1
201801_s_at	2.15	gb:AF079117.1 /DEF=Homo sapiens equilibrative NBMPR-sensitive nucleoside transporter (ENT1) mRNA, complete cds. /FEA=mRNA /GEN=ENT1 /PROD=equilibrative NBMPR-sensitive nucleosidetransporter /DB_XREF=gi:3694939 /UG=Hs.25450 solute carrier family 29 (nucleoside transporters), member 1 /FL=gb:BC001382.1 gb:U81375.1 gb:AF079117.1 gb:NM_004955.1
204257_at	2.14	gb:NM_021727.1 /DEF=Homo sapiens fatty acid desaturase 3 (FADS3), mRNA. /FEA=mRNA /GEN=FADS3 /PROD=fatty acid desaturase 3 /DB_XREF=gi:13375615 /UG=Hs.21765 fatty acid desaturase 3 /FL=gb:AF084560.1 gb:NM_021727.1 gb:BC004901.1 gb:AF134404.1
204604_at	2.14	gb:NM_012395.1 /DEF=Homo sapiens PFTAIRE protein kinase 1 (PFTK1), mRNA. /FEA=mRNA /GEN=PFTK1 /PROD=PFTAIRE protein kinase 1 /DB_XREF=gi:6912583 /UG=Hs.57856 PFTAIRE protein kinase 1 /FL=gb:AB020641.1 gb:NM_012395.1
65884_at	2.14	Cluster Incl. AA631254:nq81c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1158742 /clone_end=3 /gb=AA631254 /gi=2553865 /ug=Hs.4814 /len=876
212554_at	2.13	Consensus includes gb:N90755 /FEA=EST /DB_XREF=gi:1444082 /DB_XREF=est:zb22c08.s1 /CLONE=IMAGE:302798 /UG=Hs.296341 adenylyl cyclase-associated protein 2 /FL=gb:U02390.1 gb:NM_006366.1
212386_at	2.13	Consensus includes gb:BF592782 /FEA=EST /DB_XREF=gi:11685106 /DB_XREF=est:7j94d06.x1 /CLONE=IMAGE:3442594 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
209373_at	2.13	gb:BC003179.1 /DEF=Homo sapiens, clone MGC:4419, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:4419) /DB_XREF=gi:13112010 /UG=Hs.185055 BENE protein /FL=gb:BC003179.1 gb:NM_005434.1
209260_at	2.12	gb:BC000329.1 /DEF=Homo sapiens, stratifin, clone MGC:8516, mRNA, complete cds. /FEA=mRNA /PROD=stratifin /DB_XREF=gi:12653124 /UG=Hs.184510 stratifin /FL=gb:BC000329.1 gb:BC000995.2 gb:BC002995.1 gb:M93010.1 gb:AF029082.1 gb:NM_006142.1
219763_at	2.12	gb:NM_024820.1 /DEF=Homo sapiens KIAA1608 protein (KIAA1608), mRNA. /FEA=mRNA /GEN=KIAA1608 /PROD=hypothetical protein FLJ21129 /DB_XREF=gi:13449264 /UG=Hs.300842 KIAA1608 protein /FL=gb:NM_024820.1
208795_s_at	2.12	gb:D55716.1 /DEF=Human mRNA for P1cdc47, complete cds. /FEA=mRNA /GEN=P1cdc47 /PROD=P1cdc47 /DB_XREF=gi:1255616 /UG=Hs.77152 minichromosome maintenance deficient (S. cerevisiae) 7 /FL=gb:D55716.1
201231_s_at	2.12	gb:NM_001428.1 /DEF=Homo sapiens enolase 1, (alpha) (ENO1), mRNA. /FEA=mRNA /GEN=ENO1 /PROD=enolase 1, (alpha) /DB_XREF=gi:4503570 /UG=Hs.254105 enolase 1, (alpha) /FL=gb:BC001810.1 gb:BC004458.1 gb:M14328.1 gb:NM_001428.1
206595_at	2.11	gb:NM_001323.1 /DEF=Homo sapiens cystatin EM (CST6), mRNA. /FEA=mRNA /GEN=CST6 /PROD=cystatin M

		/DB_XREF=gi:4503112 /UG=Hs.83393 cystatin EM /FL=gb:U62800.1 gb:U81233.1 gb:NM_001323.1
220607_x_at	2.11	gb:NM_016397.1 /DEF=Homo sapiens TH1 drosophila homolog (HSPC130), mRNA. /FEA=mRNA /GEN=HSPC130 /PROD=TH1 drosophila homolog /DB_XREF=gi:7705462 /UG=Hs.5184 TH1 drosophila homolog /FL=gb:AF161479.1 gb:NM_016397.1
211066_x_at	2.1	gb:BC006439.1 /DEF=Homo sapiens, Similar to protocadherin gamma subfamily A, 5, clone MGC:13163, mRNA, complete cds. /FEA=mRNA /PROD=Similar to protocadherin gamma subfamily A, 5 /DB_XREF=gi:13623638 /FL=gb:BC006439.1
1053_at	2.1	M87338 /FEATURE= /DEFINITION=HUMA1SBU Human replication factor C, 40-kDa subunit (A1) mRNA, complete cds
213008_at	2.09	Consensus includes gb:BG403615 /FEA=EST /DB_XREF=gi:13297063 /DB_XREF=est:602419331F1 /CLONE=IMAGE:4526406 /UG=Hs.80961 polymerase (DNA directed), gamma
210517_s_at	2.09	gb:AB003476.1 /DEF=Homo sapiens mRNA for gravin, complete cds. /FEA=mRNA /PROD=gravin /DB_XREF=gi:2081606 /UG=Hs.788 A kinase (PRKA) anchor protein (gravin) 12 /FL=gb:AB003476.1
209204_at	2.08	Consensus includes gb:AI824831 /FEA=EST /DB_XREF=gi:5445502 /DB_XREF=est:wb02d08.x1 /CLONE=IMAGE:2304495 /UG=Hs.3844 LIM domain only 4 /FL=gb:BC003600.1 gb:U24576.1 gb:NM_006769.2
222036_s_at	2.08	Consensus includes gb:AI859865 /FEA=EST /DB_XREF=gi:5513481 /DB_XREF=est:wm21f03.x1 /CLONE=IMAGE:2436605 /UG=Hs.154443 minichromosome maintenance deficient (S. cerevisiae) 4
213007_at	2.08	Consensus includes gb:W74442 /FEA=EST /DB_XREF=gi:1384777 /DB_XREF=est:zd75e09.s1 /CLONE=IMAGE:346504 /UG=Hs.80961 polymerase (DNA directed), gamma
215280_s_at	2.08	Consensus includes gb:AK023850.1 /DEF=Homo sapiens cDNA FLJ13788 fis, clone SKNMC1000046, highly similar to Homo sapiens liprin-alpha3 mRNA. /FEA=mRNA /DB_XREF=gi:10435912 /UG=Hs.109299 protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3
210978_s_at	2.07	gb:BC002616.1 /DEF=Homo sapiens, transgelin 2, clone MGC:2989, mRNA, complete cds. /FEA=mRNA /PROD=transgelin 2 /DB_XREF=gi:12803566 /UG=Hs.75725 transgelin 2 /FL=gb:BC002616.1
216242_x_at	2.07	Consensus includes gb:AW402635 /FEA=EST /DB_XREF=gi:6921341 /DB_XREF=est:UI-HF-BK0-aav-a-09-0-UI.r1 /CLONE=IMAGE:3055001 /UG=Hs.80475 polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
210830_s_at	2.07	gb:AF001602.1 /DEF=Homo sapiens paraoxonase (PON2) mRNA, with alternatively spliced exon 3, complete cds. /FEA=mRNA /GEN=PON2 /PROD=paraoxonase /DB_XREF=gi:2228776 /UG=Hs.169857 paraoxonase 2 /FL=gb:AF001602.1
212624_s_at	2.06	Consensus includes gb:BF339445 /FEA=EST /DB_XREF=gi:11285900 /DB_XREF=est:602038795F1 /CLONE=IMAGE:4186582 /UG=Hs.169965 chimerin (chimaerin) 1
221830_at	2.06	Consensus includes gb:AI302106 /FEA=EST /DB_XREF=gi:3961452 /DB_XREF=est:qn57h10.x1 /CLONE=IMAGE:1902403 /UG=Hs.301746 RAP2A, member of RAS oncogene family /FL=gb:NM_021033.1
217388_s_at	2.06	Consensus includes gb:D55639.1 /DEF=Human monocyte PABL (pseudoautosomal boundary-like sequence) mRNA, clone Mo1. /FEA=mRNA /DB_XREF=gi:1255614 /UG=Hs.169139 kynureninase (L-kynurenine hydrolase)
207943_x_at	2.06	gb:NM_006718.1 /DEF=Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA. /FEA=mRNA /GEN=PLAGL1 /PROD=pleiomorphic adenoma gene-like 1 isoform 2 /DB_XREF=gi:6031193 /UG=Hs.75825 pleiomorphic adenoma gene-like 1 /FL=gb:NM_006718.1
208336_s_at	2.06	gb:NM_004868.1 /DEF=Homo sapiens glycoprotein, synaptic 2 (GPSN2), mRNA. /FEA=mRNA /GEN=GPSN2 /PROD=glycoprotein, synaptic 2 /DB_XREF=gi:4759061 /UG=Hs.306122 glycoprotein, synaptic 2 /FL=gb:AF038959.1 gb:NM_004868.1
AFFX-r2-Hs18SrRNA-	2.05	M10098 Human 18S rRNA sequence, length 1969 bases, 3 prime target bases 1293-1938

3_s_at		
212625_at	2.05	Consensus includes gb:NM_003765.1 /DEF=Homo sapiens syntaxin 10 (STX10), mRNA. /FEA=CDS /GEN=STX10 /PROD=syntaxin 10 /DB_XREF=gi:4507284 /UG=Hs.43812 syntaxin 10 /FL=gb:AF035531.1 gb:NM_003765.1
205588_s_at	2.05	gb:NM_007045.1 /DEF=Homo sapiens FGFR1 oncogene partner (FOP), mRNA. /FEA=mRNA /GEN=FOP /PROD=FGFR1 oncogene partner /DB_XREF=gi:5901953 /UG=Hs.180296 FGFR1 oncogene partner /FL=gb:NM_007045.1
219493_at	2.04	gb:NM_024745.1 /DEF=Homo sapiens hypothetical protein FLJ22009 (FLJ22009), mRNA. /FEA=mRNA /GEN=FLJ22009 /PROD=hypothetical protein FLJ22009 /DB_XREF=gi:13376069 /UG=Hs.123253 hypothetical protein FLJ22009 /FL=gb:NM_024745.1
218111_s_at	2.04	gb:NM_018686.1 /DEF=Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA. /FEA=mRNA /GEN=LOC55907 /PROD=CMP-N-acetylneuraminic acid synthase /DB_XREF=gi:8923899 /UG=Hs.12492 CMP-N-acetylneuraminic acid synthase /FL=gb:AF271388.1 gb:NM_018686.1
202954_at	2.04	gb:NM_007019.1 /DEF=Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA. /FEA=mRNA /GEN=UBCH10 /PROD=ubiquitin carrier protein E2-C /DB_XREF=gi:5902145 /UG=Hs.93002 ubiquitin carrier protein E2-C /FL=gb:U73379.1 gb:NM_007019.1
214679_x_at	2.04	Consensus includes gb:AL110227.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434J194 (from clone DKFZp434J194). /FEA=mRNA /DB_XREF=gi:5817165 /UG=Hs.323067 Homo sapiens mRNA; cDNA DKFZp434J194 (from clone DKFZp434J194)
207163_s_at	2.04	gb:NM_005163.1 /DEF=Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), mRNA. /FEA=mRNA /GEN=AKT1 /PROD=serinethreonine protein kinase /DB_XREF=gi:4885060 /UG=Hs.71816 v-akt murine thymoma viral oncogene homolog 1 /FL=gb:M63167.1 gb:NM_005163.1
58696_at	2.03	Cluster Incl. AL039469:DKFZp434P0110_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434P0110 /clone_end=3 /gb=AL039469 /gi=5408517 /ug=Hs.97574 /len=888
210983_s_at	2.03	gb:AF279900.1 /DEF=Homo sapiens PNAS-146 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-146 /DB_XREF=gi:12751125 /UG=Hs.77152 minichromosome maintenance deficient (S. cerevisiae) 7 /FL=gb:AF279900.1
201490_s_at	2.03	gb:NM_005729.1 /DEF=Homo sapiens peptidylprolyl isomerase F (cyclophilin F) (PPIF), mRNA. /FEA=mRNA /GEN=PPIF /PROD=peptidylprolyl isomerase F (cyclophilin F) /DB_XREF=gi:5031986 /UG=Hs.173125 peptidylprolyl isomerase F (cyclophilin F) /FL=gb:BC005020.1 gb:M80254.1 gb:NM_005729.1
218069_at	2.03	gb:NM_024096.1 /DEF=Homo sapiens hypothetical protein MGC5627 (MGC5627), mRNA. /FEA=mRNA /GEN=MGC5627 /PROD=hypothetical protein MGC5627 /DB_XREF=gi:13129099 /UG=Hs.237971 hypothetical protein MGC5627 /FL=gb:BC001344.1 gb:NM_024096.1 gb:AF212242.1
211065_x_at	2.02	gb:BC006422.1 /DEF=Homo sapiens, clone MGC:12724, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:12724) /DB_XREF=gi:13623608 /FL=gb:BC006422.1
204949_at	2.02	gb:NM_002162.2 /DEF=Homo sapiens intercellular adhesion molecule 3 (ICAM3), mRNA. /FEA=mRNA /GEN=ICAM3 /PROD=intercellular adhesion molecule 3 precursor /DB_XREF=gi:12545399 /UG=Hs.99995 intercellular adhesion molecule 3 /FL=gb:NM_002162.2
202094_at	2.02	Consensus includes gb:AA648913 /FEA=EST /DB_XREF=gi:2575342 /DB_XREF=est:ns41a09.s1 /CLONE=IMAGE:1186168 /UG=Hs.1578 baculoviral IAP repeat-containing 5 (survivin) /FL=gb:NM_001168.1 gb:AF077350.1
221676_s_at	2.01	gb:BC002342.1 /DEF=Homo sapiens, coronin, actin-binding protein, 1C, clone MGC:8518, mRNA, complete cds. /FEA=mRNA /PROD=coronin, actin-binding protein, 1C /DB_XREF=gi:12803080 /UG=Hs.17377 coronin, actin-binding protein, 1C /FL=gb:BC002342.1

209191_at	2.01	gb:BC002654.1 /DEF=Homo sapiens, Similar to tubulin, beta, 4, clone MGC:4083, mRNA, complete cds. /FEA=mRNA /PROD=Similar to tubulin, beta, 4 /DB_XREF=gi:12803638 /UG=Hs.274398 Homo sapiens, Similar to tubulin, beta, 4, clone MGC:4083, mRNA, complete cds /FL=gb:BC002654.1
200661_at	2	gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) /FL=gb:BC000597.1 gb:M22960.1 gb:NM_000308.1
211676_s_at	2	gb:AF056979.1 /DEF=Homo sapiens clone YAN1 interferon-gamma receptor mRNA, complete cds. /FEA=mRNA /PROD=interferon-gamma receptor /DB_XREF=gi:13562048 /FL=gb:AF056979.1
205199_at	2	gb:NM_001216.1 /DEF=Homo sapiens carbonic anhydrase IX (CA9), mRNA. /FEA=mRNA /GEN=CA9 /PROD=carbonic anhydrase IX precursor /DB_XREF=gi:9955947 /UG=Hs.63287 carbonic anhydrase IX /FL=gb:NM_001216.1
218153_at	2	gb:NM_024537.1 /DEF=Homo sapiens hypothetical protein FLJ12118 (FLJ12118), mRNA. /FEA=mRNA /GEN=FLJ12118 /PROD=hypothetical protein FLJ12118 /DB_XREF=gi:13375694 /UG=Hs.7779 hypothetical protein FLJ12118 /FL=gb:NM_024537.1
220272_at	2	gb:NM_017637.1 /DEF=Homo sapiens hypothetical protein FLJ20043 (FLJ20043), mRNA. /FEA=mRNA /GEN=FLJ20043 /PROD=hypothetical protein FLJ20043 /DB_XREF=gi:8923050 /UG=Hs.103853 hypothetical protein FLJ20043 /FL=gb:NM_017637.1
200788_s_at	2	gb:NM_003768.1 /DEF=Homo sapiens phosphoprotein enriched in astrocytes 15 (PEA15), mRNA. /FEA=mRNA /GEN=PEA15 /PROD=phosphoprotein enriched in astrocytes 15 /DB_XREF=gi:4505704 /UG=Hs.194673 phosphoprotein enriched in astrocytes 15 /FL=gb:BC002426.1 gb:NM_003768.1
208611_s_at	1.99	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805279 /UG=Hs.77196 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1
201819_at	1.99	gb:NM_005505.1 /DEF=Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (CD36L1), mRNA. /FEA=mRNA /GEN=CD36L1 /PROD=CD36 antigen (collagen type I receptor,thrombospondin receptor)-like 1 /DB_XREF=gi:5031628 /UG=Hs.180616 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 /FL=gb:NM_005505.1
213951_s_at	1.98	Consensus includes gb:BE964655 /FEA=EST /DB_XREF=gi:11768198 /DB_XREF=est:601658585R1 /CLONE=IMAGE:3885812 /UG=Hs.78185 MAX-like bHLHZIP protein
222047_s_at	1.97	Consensus includes gb:AI523895 /FEA=EST /DB_XREF=gi:4438030 /DB_XREF=est:tg97g03.x1 /CLONE=IMAGE:2116756 /UG=Hs.111801 arsenate resistance protein ARS2
203454_s_at	1.97	gb:NM_004045.1 /DEF=Homo sapiens ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1), mRNA. /FEA=mRNA /GEN=ATOX1 /PROD=ATX1 (antioxidant protein 1, yeast) homolog 1 /DB_XREF=gi:4757803 /UG=Hs.279910 ATX1 (antioxidant protein 1, yeast) homolog 1 /FL=gb:NM_004045.1
207002_s_at	1.96	gb:NM_002656.1 /DEF=Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 1, mRNA. /FEA=mRNA /GEN=PLAGL1 /PROD=pleiomorphic adenoma gene-like 1 isoform 1 /DB_XREF=gi:4505856 /UG=Hs.75825 pleiomorphic adenoma gene-like 1 /FL=gb:U81992.1 gb:NM_002656.1
200997_at	1.96	gb:NM_002896.1 /DEF=Homo sapiens RNA binding motif protein 4 (RBM4), mRNA. /FEA=mRNA /GEN=RBM4 /PROD=RNA binding motif protein 4 /DB_XREF=gi:4506444 /UG=Hs.6106 RNA binding motif protein 4 /FL=gb:BC000307.1 gb:U89505.1 gb:NM_002896.1
217934_x_at	1.96	gb:NM_005861.1 /DEF=Homo sapiens STIP1 homology and U-Box containing protein 1 (STUB1), mRNA. /FEA=mRNA /GEN=STUB1 /PROD=serologically defined colon cancer antigen 7 /DB_XREF=gi:5031962

		/UG=Hs.25197 STIP1 homology and U-Box containing protein 1 /FL=gb:AF039689.1 gb:AF129085.1 gb:NM_005861.1
219068_x_at	1.96	gb:NM_018188.1 /DEF=Homo sapiens hypothetical protein FLJ10709 (FLJ10709), mRNA. /FEA=mRNA /GEN=FLJ10709 /PROD=hypothetical protein FLJ10709 /DB_XREF=gi:8922608 /UG=Hs.273357 hypothetical protein FLJ10709 /FL=gb:NM_018188.1
206022_at	1.96	gb:NM_000266.1 /DEF=Homo sapiens Norrie disease (pseudoglioma) (NDP), mRNA. /FEA=mRNA /GEN=NDP /PROD=Norrie disease protein /DB_XREF=gi:4557788 /UG=Hs.2839 Norrie disease (pseudoglioma) /FL=gb:NM_000266.1
200621_at	1.96	gb:NM_004078.1 /DEF=Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA. /FEA=mRNA /GEN=CSRP1 /PROD=cysteine and glycine-rich protein 1 /DB_XREF=gi:4758085 /UG=Hs.108080 cysteine and glycine-rich protein 1 /FL=gb:M33146.1 gb:NM_004078.1
209172_s_at	1.95	gb:U30872.1 /DEF=Human mitosin mRNA, complete cds. /FEA=mRNA /PROD=mitosin /DB_XREF=gi:1000093 /UG=Hs.77204 centromere protein F (350400kD, mitosin) /FL=gb:U30872.1
221704_s_at	1.95	gb:BC005882.1 /DEF=Homo sapiens, hypothetical protein FLJ12750, clone MGC:4691, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ12750 /DB_XREF=gi:13543447 /FL=gb:BC005882.1
208622_s_at	1.94	Consensus includes gb:AA670344 /FEA=EST /DB_XREF=gi:2631843 /DB_XREF=est:ad16b08.s1 /CLONE=IMAGE:878391 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:NM_003379.2
201895_at	1.94	gb:NM_001654.1 /DEF=Homo sapiens v-raf murine sarcoma 3611 viral oncogene homolog 1 (ARAF1), mRNA. /FEA=mRNA /GEN=ARAF1 /PROD=v-raf murine sarcoma 3611 viral oncogene homolog1 /DB_XREF=gi:4502192 /UG=Hs.77183 v-raf murine sarcoma 3611 viral oncogene homolog 1 /FL=gb:BC002466.1 gb:NM_001654.1
207980_s_at	1.94	gb:NM_006079.1 /DEF=Homo sapiens Cbpp300-interacting transactivator, with GluAsp-rich carboxy-terminal domain, 2 (CITED2), mRNA. /FEA=mRNA /GEN=CITED2 /PROD=Cbpp300-interacting transactivator, withGluAsp-rich carboxy-terminal domain, 2 /DB_XREF=gi:5174416 /UG=Hs.82071 Cbpp300-interacting transactivator, with GluAsp-rich carboxy-terminal domain, 2 /FL=gb:U65093.1 gb:NM_006079.1
203572_s_at	1.94	gb:NM_005641.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 7085kD (TAF2E), mRNA. /FEA=mRNA /GEN=TAF2E /PROD=TATA box binding protein (TBP)-associatedfactor, RNA polymerase II, E, 7085kD /DB_XREF=gi:5032146 /UG=Hs.78865 TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 7085kD /FL=gb:NM_005641.1 gb:L25444.1
202725_at	1.94	gb:NM_000937.1 /DEF=Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A), mRNA. /FEA=mRNA /GEN=POLR2A /PROD=polymerase (RNA) II (DNA directed) polypeptide A(220kD) /DB_XREF=gi:4505938 /UG=Hs.171880 polymerase (RNA) II (DNA directed) polypeptide A (220kD) /FL=gb:NM_000937.1
212722_s_at	1.94	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FLJ11718 fis, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIAA0585 protein. /FEA=mRNA /DB_XREF=gi:10433034 /UG=Hs.72660 phosphatidylserine receptor
201999_s_at	1.93	gb:NM_006519.1 /DEF=Homo sapiens t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA. /FEA=mRNA /GEN=TCTEL1 /PROD=t-complex-associated-testis-expressed 1-like 1 /DB_XREF=gi:5730084 /UG=Hs.266940 t-complex-associated-testis-expressed 1-like 1 /FL=gb:U56255.1 gb:D50663.1 gb:NM_006519.1
200884_at	1.93	gb:NM_001823.1 /DEF=Homo sapiens creatine kinase, brain (CKB), mRNA. /FEA=mRNA /GEN=CKB /PROD=creatine kinase, brain /DB_XREF=gi:4502850 /UG=Hs.173724 creatine kinase, brain /FL=gb:L47647.1 gb:BC001190.1 gb:BC004914.1 gb:M16364.1 gb:M16451.1 gb:NM_001823.1
202292_x_at	1.93	gb:NM_007260.1 /DEF=Homo sapiens lysophospholipase II (LYPLA2), mRNA. /FEA=mRNA /GEN=LYPLA2 /PROD=lysophospholipase II /DB_XREF=gi:9966763 /UG=Hs.283655 lysophospholipase II /FL=gb:AF098668.1

		gb:NM_007260.1
209774_x_at	1.93	gb:M57731.1 /DEF=Human gro-beta mRNA, complete cds. /FEA=mRNA /GEN=gro-beta /PROD=cytokine gro-beta /DB_XREF=gi:183626 /UG=Hs.75765 GRO2 oncogene /FL=gb:M57731.1 gb:M36820.1 gb:NM_002089.1
202819_s_at	1.92	gb:NM_003198.1 /DEF=Homo sapiens transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) (TCEB3), mRNA. /FEA=mRNA /GEN=TCEB3 /PROD=elongin A /DB_XREF=gi:4507388 /UG=Hs.155202 transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A) /FL=gb:BC002883.1 gb:NM_003198.1 gb:L47345.1
205345_at	1.91	gb:NM_000465.1 /DEF=Homo sapiens BRCA1 associated RING domain 1 (BARD1), mRNA. /FEA=mRNA /GEN=BARD1 /PROD=BRCA1 associated RING domain 1 /DB_XREF=gi:4557348 /UG=Hs.54089 BRCA1 associated RING domain 1 /FL=gb:U76638.1 gb:NM_000465.1
207876_s_at	1.91	gb:NM_001458.1 /DEF=Homo sapiens filamin C, gamma (actin-binding protein-280) (FLNC), mRNA. /FEA=mRNA /GEN=FLNC /PROD=gamma filamin /DB_XREF=gi:4557596 /UG=Hs.58414 filamin C, gamma (actin-binding protein-280) /FL=gb:AF089841.1 gb:NM_001458.1
202945_at	1.9	gb:NM_004957.1 /DEF=Homo sapiens folylpolyglutamate synthase (FPGS), mRNA. /FEA=mRNA /GEN=FPGS /PROD=folylpolyglutamate synthase /DB_XREF=gi:4826727 /UG=Hs.754 folylpolyglutamate synthase /FL=gb:M98045.1 gb:NM_004957.1
205352_at	1.9	gb:NM_005025.1 /DEF=Homo sapiens protease inhibitor 12 (neuroserpin) (SERPINI1), mRNA. /FEA=mRNA /GEN=SERPINI1 /PROD=protease inhibitor 12 (neuroserpin) /DB_XREF=gi:4826903 /UG=Hs.78589 serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 /FL=gb:NM_005025.1
221591_s_at	1.9	gb:BC005004.1 /DEF=Homo sapiens, hypothetical protein FLJ10491, clone MGC:961, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ10491 /DB_XREF=gi:13436475 /UG=Hs.86211 hypothetical protein /FL=gb:BC005004.1
212788_x_at	1.9	Consensus includes gb:BG537190 /FEA=EST /DB_XREF=gi:13528922 /DB_XREF=est:602565589F1 /CLONE=IMAGE:4690079 /UG=Hs.111334 ferritin, light polypeptide
210933_s_at	1.89	gb:BC004908.1 /DEF=Homo sapiens, clone MGC:4655, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:4655) /DB_XREF=gi:13436196 /UG=Hs.326737 Homo sapiens, clone MGC:4655, mRNA, complete cds /FL=gb:BC004908.1
217907_at	1.88	gb:NM_014161.1 /DEF=Homo sapiens HSPC071 protein (HSPC071), mRNA. /FEA=mRNA /GEN=HSPC071 /PROD=HSPC071 protein /DB_XREF=gi:7661777 /UG=Hs.23038 HSPC071 protein /FL=gb:AL136633.1 gb:BC001623.1 gb:AF161556.1 gb:NM_014161.1
211126_s_at	1.88	gb:U46006.1 /DEF=Homo sapiens smooth muscle LIM protein (h-SmLIM) mRNA, complete cds. /FEA=mRNA /GEN=h-SmLIM /PROD=smooth muscle LIM protein /DB_XREF=gi:1314358 /UG=Hs.10526 cysteine and glycine-rich protein 2 /FL=gb:U46006.1
220757_s_at	1.88	gb:NM_025241.1 /DEF=Homo sapiens UBX domain-containing gene 1 (UBXD1), mRNA. /FEA=mRNA /GEN=UBXD1 /PROD=UBX domain-containing gene 1 /DB_XREF=gi:13376853 /UG=Hs.11081 UBX domain-containing 2 /FL=gb:AF272893.1 gb:NM_025241.1
209478_at	1.88	gb:U95006.1 /DEF=Human D9 splice variant A mRNA, complete cds. /FEA=mRNA /PROD=D9 splice variant A /DB_XREF=gi:2071992 /UG=Hs.37616 Human D9 splice variant B mRNA, complete cds /FL=gb:U95006.1 gb:U95007.1
202275_at	1.87	gb:NM_000402.1 /DEF=Homo sapiens glucose-6-phosphate dehydrogenase (G6PD), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=G6PD /PROD=glucose-6-phosphate dehydrogenase /DB_XREF=gi:4503844 /UG=Hs.80206 glucose-6-phosphate dehydrogenase /FL=gb:BC000337.1 gb:M21248.1 gb:NM_000402.1

203085_s_at	1.85	gb:BC000125.1 /DEF=Homo sapiens, Similar to transforming growth factor, beta 1, clone MGC:3119, mRNA, complete cds. /FEA=mRNA /PROD=Similar to transforming growth factor, beta 1 /DB_XREF=gi:12652748 /UG=Hs.1103 transforming growth factor, beta 1 /FL=gb:NM_000660.1 gb:BC000125.1 gb:BC001180.1 gb:M38449.1
215566_x_at	1.85	Consensus includes gb:AK024724.1 /DEF=Homo sapiens cDNA: FLJ21071 fis, clone CAS01789, highly similar to AF098668 Homo sapiens acyl-protein thioesterase mRNA. /FEA=mRNA /DB_XREF=gi:10437080 /UG=Hs.283655 lysophospholipase II
202207_at	1.85	Consensus includes gb:BG435404 /FEA=EST /DB_XREF=gi:13341910 /DB_XREF=est:602507678F1 /CLONE=IMAGE:4605066 /UG=Hs.111554 ADP-ribosylation factor-like 7 /FL=gb:BC001051.1 gb:AB016811.1 gb:NM_005737.2
201976_s_at	1.84	gb:NM_012334.1 /DEF=Homo sapiens myosin X (MYO10), mRNA. /FEA=mRNA /GEN=MYO10 /PROD=myosin X /DB_XREF=gi:11037056 /UG=Hs.61638 myosin X /FL=gb:NM_012334.1 gb:AF234532.1 gb:AF247457.2
211814_s_at	1.82	gb:AF112857.1 /DEF=Homo sapiens cyclin E2 splice variant 1 mRNA, complete cds. /FEA=CDS /PROD=cyclin E2 splice variant 1 /DB_XREF=gi:4092787 /UG=Hs.30464 cyclin E2 /FL=gb:AF112857.1
206593_s_at	1.79	gb:NM_006752.1 /DEF=Homo sapiens surfeit 5 (SURF5), mRNA. /FEA=mRNA /GEN=SURF5 /PROD=surfeit 5 /DB_XREF=gi:5803182 /UG=Hs.78354 surfeit 5 /FL=gb:NM_006752.1
221436_s_at	1.78	gb:NM_031299.1 /DEF=Homo sapiens hypothetical protein MGC2577 (MGC2577), mRNA. /FEA=CDS /GEN=MGC2577 /PROD=hypothetical protein MGC2577 /DB_XREF=gi:13876383 /FL=gb:NM_031299.1
201645_at	1.78	gb:NM_002160.1 /DEF=Homo sapiens hexabrachion (tenascin C, cytotactin) (HXB), mRNA. /FEA=mRNA /GEN=HXB /PROD=hexabrachion (tenascin C, cytotactin) /DB_XREF=gi:4504548 /UG=Hs.289114 hexabrachion (tenascin C, cytotactin) /FL=gb:M55618.1 gb:NM_002160.1
209053_s_at	1.78	Consensus includes gb:BE793789 /FEA=EST /DB_XREF=gi:10214987 /DB_XREF=est:601589946F1 /CLONE=IMAGE:3944195 /UG=Hs.110457 Wolf-Hirschhorn syndrome candidate 1 /FL=gb:AF083389.1
204214_s_at	1.78	gb:NM_006834.1 /DEF=Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA. /FEA=mRNA /GEN=RAB32 /PROD=RAB32, member RAS oncogene family /DB_XREF=gi:5803132 /UG=Hs.32217 RAB32, member RAS oncogene family /FL=gb:U71127.1 gb:NM_006834.1
215047_at	1.77	Consensus includes gb:AL080170.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434C091 (from clone DKFZp434C091); partial cds. /FEA=mRNA /GEN=DKFZp434C091 /PROD=hypothetical protein /DB_XREF=gi:5262639 /UG=Hs.51692 DKFZP434C091 protein
211535_s_at	1.77	gb:M60485.1 /DEF=Human fibroblast growth factor receptor mRNA, complete cds. /FEA=mRNA /PROD=fibroblast growth factor receptor /DB_XREF=gi:182560 /UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) /FL=gb:M60485.1
213668_s_at	1.77	Consensus includes gb:AI989477 /FEA=EST /DB_XREF=gi:5836358 /DB_XREF=est:ws25b11.x1 /CLONE=IMAGE:2498205 /UG=Hs.83484 SRY (sex determining region Y)-box 4
202407_s_at	1.77	Consensus includes gb:BF342707 /FEA=EST /DB_XREF=gi:11289729 /DB_XREF=est:602013660F1 /CLONE=IMAGE:4149542 /UG=Hs.183438 DKFZP566J153 protein /FL=gb:AL050369.1 gb:NM_015629.1
213646_x_at	1.77	Consensus includes gb:BE300252 /FEA=EST /DB_XREF=gi:9184000 /DB_XREF=est:600944004T1 /CLONE=IMAGE:2960280 /UG=Hs.240615 hypothetical protein FLJ13556 similar to N-myc downstream regulated 3
213147_at	1.77	Consensus includes gb:AI375919 /FEA=EST /DB_XREF=gi:4175909 /DB_XREF=est:tc14d04.x1 /CLONE=IMAGE:2063815 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1
222043_at	1.75	Consensus includes gb:AI982754 /FEA=EST /DB_XREF=gi:5809973 /DB_XREF=est:wz28g10.x1 /CLONE=IMAGE:2559426 /UG=Hs.75106 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2,

		testosterone-repressed prostate message 2, apolipoprotein J)
215537_x_at	1.74	Consensus includes gb:AJ012008 /DEF=Homo sapiens genes encoding RNCC protein, DDAH protein, Ly6-C protein, Ly6-D protein and immunoglobulin receptor /FEA=mRNA_4 /DB_XREF=gi:5304874 /UG=Hs.247362 dimethylarginine dimethylaminohydrolase 2
203175_at	1.74	gb:NM_001665.1 /DEF=Homo sapiens ras homolog gene family, member G (rho G) (ARHG), mRNA. /FEA=mRNA /GEN=ARHG /PROD=ras homolog gene family, member G (rho G) /DB_XREF=gi:4502218 /UG=Hs.75082 ras homolog gene family, member G (rho G) /FL=gb:NM_001665.1
200959_at	1.74	gb:NM_004960.1 /DEF=Homo sapiens fusion, derived from t(12;16) malignant liposarcoma (FUS), mRNA. /FEA=mRNA /GEN=FUS /PROD=fusion, derived from t(12;16) malignantliposarcoma /DB_XREF=gi:4826733 /UG=Hs.99969 fusion, derived from t(12;16) malignant liposarcoma /FL=gb:BC000402.1 gb:BC002459.1 gb:NM_004960.1
216228_s_at	1.72	Consensus includes gb:AK001538.1 /DEF=Homo sapiens cDNA FLJ10676 fis, clone NT2RP2006464, highly similar to Homo sapiens mRNA for AND-1 protein. /FEA=mRNA /DB_XREF=gi:7022855 /UG=Hs.72160 AND-1 protein
204998_s_at	1.72	gb:NM_012068.2 /DEF=Homo sapiens activating transcription factor 5 (ATF5), mRNA. /FEA=mRNA /GEN=ATF5 /PROD=activating transcription factor 5 /DB_XREF=gi:12597624 /UG=Hs.9754 activating transcription factor 5 /FL=gb:AF305687.1 gb:AB021663.2 gb:NM_012068.2 gb:BC005174.1
201949_x_at	1.71	Consensus includes gb:AL572341 /FEA=EST /DB_XREF=gi:12930514 /DB_XREF=est:AL572341 /CLONE=CS0DI007YC13 (3 prime) /UG=Hs.76368 capping protein (actin filament) muscle Z-line, beta /FL=gb:NM_004930.1 gb:U03271.1
218105_s_at	1.65	gb:NM_015956.1 /DEF=Homo sapiens CGI-28 protein (LOC51073), mRNA. /FEA=mRNA /GEN=LOC51073 /PROD=CGI-28 protein /DB_XREF=gi:7705721 /UG=Hs.279652 CGI-28 protein /FL=gb:AF132962.1 gb:NM_015956.1
212203_x_at	1.59	Consensus includes gb:BF338947 /FEA=EST /DB_XREF=gi:11285367 /DB_XREF=est:602036012F1 /CLONE=IMAGE:4184090 /UG=Hs.182241 interferon induced transmembrane protein 3 (1-8U)
201427_s_at	1.56	gb:NM_005410.1 /DEF=Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA. /FEA=mRNA /GEN=SEPP1 /PROD=selenoprotein P precursor /DB_XREF=gi:4885590 /UG=Hs.3314 selenoprotein P, plasma, 1 /FL=gb:NM_005410.1
217729_s_at	1.49	gb:NM_001130.3 /DEF=Homo sapiens amino-terminal enhancer of split (AES), mRNA. /FEA=mRNA /GEN=AES /PROD=amino-terminal enhancer of split /DB_XREF=gi:6382065 /UG=Hs.244 amino-terminal enhancer of split /FL=gb:AF072902.1 gb:U04241.1 gb:NM_001130.3
212518_at	1.4	Consensus includes gb:AB011161.1 /DEF=Homo sapiens mRNA for KIAA0589 protein, partial cds. /FEA=mRNA /GEN=KIAA0589 /PROD=KIAA0589 protein /DB_XREF=gi:3043701 /UG=Hs.275182 phosphatidylinositol-4-phosphate 5-kinase, type I, gamma
206482_at	-1.4	gb:NM_005975.1 /DEF=Homo sapiens PTK6 protein tyrosine kinase 6 (PTK6), mRNA. /FEA=mRNA /GEN=PTK6 /PROD=PTK6 protein tyrosine kinase 6 /DB_XREF=gi:5174646 /UG=Hs.51133 PTK6 protein tyrosine kinase 6 /FL=gb:NM_005975.1
211959_at	-1.44	Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE=IMAGE:2500861 /UG=Hs.103391 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA
204276_at	-1.47	Consensus includes gb:BE895437 /FEA=EST /DB_XREF=gi:10358829 /DB_XREF=est:601437912F1 /CLONE=IMAGE:3922971 /UG=Hs.274701 thymidine kinase 2, mitochondrial /FL=gb:NM_004614.1 gb:U77088.1
209538_at	-1.5	gb:U69645.1 /DEF=Human zinc finger protein mRNA, complete cds. /FEA=mRNA /PROD=zinc finger protein /DB_XREF=gi:1575614 /UG=Hs.78765 zinc finger protein 32 (KOX 30) /FL=gb:U69645.1

201831_s_at	-1.55	Consensus includes gb:BE875592 /FEA=EST /DB_XREF=gi:10324368 /DB_XREF=est:601487031F1 /CLONE=IMAGE:3889710 /UG=Hs.325948 vesicle docking protein p115 /FL=gb:D86326.1 gb:NM_003715.1
218769_s_at	-1.57	gb:NM_023039.1 /DEF=Homo sapiens ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA. /FEA=mRNA /GEN=ANKRA2 /PROD=ankyrin repeat, family A (RFXANK-like), 2 /DB_XREF=gi:12746411 /UG=Hs.239154 ankyrin repeat, family A (RFXANK-like), 2 /FL=gb:AF314032.1 gb:NM_023039.1
206668_s_at	-1.61	gb:NM_004866.1 /DEF=Homo sapiens secretory carrier membrane protein 1 (SCAMP1), mRNA. /FEA=mRNA /GEN=SCAMP1 /PROD=secretory carrier membrane protein 1 /DB_XREF=gi:4759063 /UG=Hs.31218 secretory carrier membrane protein 1 /FL=gb:AF005037.1 gb:AF038966.1 gb:NM_004866.1
218383_at	-1.62	gb:NM_017815.1 /DEF=Homo sapiens hypothetical protein FLJ20424 (FLJ20424), mRNA. /FEA=mRNA /GEN=FLJ20424 /PROD=hypothetical protein FLJ20424 /DB_XREF=gi:8923395 /UG=Hs.8886 hypothetical protein FLJ20424 /FL=gb:BC002554.1 gb:BC001916.1 gb:NM_017815.1
203711_s_at	-1.66	gb:NM_014362.1 /DEF=Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA. /FEA=mRNA /GEN=HIBCH /PROD=3-hydroxyisobutyryl-Coenzyme A hydrolase /DB_XREF=gi:7657159 /UG=Hs.236642 3-hydroxyisobutyryl-Coenzyme A hydrolase /FL=gb:BC005190.1 gb:U66669.1 gb:NM_014362.1
218764_at	-1.68	gb:NM_024064.1 /DEF=Homo sapiens hypothetical protein MGC5363 (MGC5363), mRNA. /FEA=mRNA /GEN=MGC5363 /PROD=hypothetical protein MGC5363 /DB_XREF=gi:13129041 /UG=Hs.1880 hypothetical protein MGC5363 /FL=gb:BC001000.2 gb:NM_024064.1
213605_s_at	-1.7	Consensus includes gb:AL049987.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112). /FEA=mRNA /DB_XREF=gi:4884238 /UG=Hs.166361 Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)
211812_s_at	-1.73	gb:AB050856.1 /DEF=Homo sapiens beta3GalNAcT-1 mRNA for globoside synthase, complete cds, clone:type 2. /FEA=CDS /GEN=beta3GalNAcT-1 /PROD=globoside synthase /DB_XREF=gi:11136456 /UG=Hs.267695 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3 /FL=gb:AB050856.1
215221_at	-1.74	Consensus includes gb:AK025064.1 /DEF=Homo sapiens cDNA: FLJ21411 fis, clone COL03986. /FEA=mRNA /DB_XREF=gi:10437503 /UG=Hs.306758 Homo sapiens cDNA: FLJ21411 fis, clone COL03986
205709_s_at	-1.77	gb:NM_001263.1 /DEF=Homo sapiens CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1 (CDS1), mRNA. /FEA=mRNA /GEN=CDS1 /PROD=CDP-diacylglycerol synthase (phosphatidatecytidylyltransferase) 1 /DB_XREF=gi:4502756 /UG=Hs.152981 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1 /FL=gb:U65887.1 gb:NM_001263.1
203166_at	-1.81	gb:NM_006324.1 /DEF=Homo sapiens craniofacial development protein 1 (CFDP1), mRNA. /FEA=mRNA /GEN=CFDP1 /PROD=craniofacial development protein 1 /DB_XREF=gi:5453566 /UG=Hs.296460 craniofacial development protein 1 /FL=gb:BC000991.2 gb:AB009285.1 gb:NM_006324.1
213073_at	-1.82	Consensus includes gb:AB002319.1 /DEF=Human mRNA for KIAA0321 gene, partial cds. /FEA=mRNA /GEN=KIAA0321 /DB_XREF=gi:2224582 /UG=Hs.8663 KIAA0321 protein
35148_at	-1.82	Cluster Incl. AC005954:Homo sapiens chromosome 19, cosmid R28784 /cds=(0,2858) /gb=AC005954 /gi=3851201 /ug=Hs.25527 /len=2859
212274_at	-1.82	Consensus includes gb:AV705559 /FEA=EST /DB_XREF=gi:10722858 /DB_XREF=est:AV705559 /CLONE=ADBAPE04 /UG=Hs.81412 lipin 1
213049_at	-1.83	Consensus includes gb:BG436400 /FEA=EST /DB_XREF=gi:13342906 /DB_XREF=est:602509062F1 /CLONE=IMAGE:4619679 /UG=Hs.167031 DKFZP566D133 protein
204203_at	-1.83	gb:NM_001806.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), gamma (CEBPG), mRNA. /FEA=mRNA /GEN=CEBPG /PROD=CCAATenhancer binding protein gamma /DB_XREF=gi:4502768 /UG=Hs.2227 CCAATenhancer binding protein (CEBP), gamma /FL=gb:NM_001806.1 gb:U20240.1

39549_at	-1.84	Cluster Incl. AI743090:wg87a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2372060 /clone_end=3 /gb=AI743090 /gi=5111378 /ug=Hs.106705 /len=547
212686_at	-1.84	Consensus includes gb:AB032983.1 /DEF=Homo sapiens mRNA for KIAA1157 protein, partial cds. /FEA=mRNA /GEN=KIAA1157 /PROD=KIAA1157 protein /DB_XREF=gi:6330128 /UG=Hs.21894 KIAA1157 protein
214077_x_at	-1.84	Consensus includes gb:H15129 /FEA=EST /DB_XREF=gi:879949 /DB_XREF=est:ym30b02.s1 /CLONE=IMAGE:49680 /UG=Hs.117313 Meis (mouse) homolog 3
200854_at	-1.85	Consensus includes gb:AB028970.1 /DEF=Homo sapiens mRNA for KIAA1047 protein, partial cds. /FEA=mRNA /GEN=KIAA1047 /PROD=KIAA1047 protein /DB_XREF=gi:5689430 /UG=Hs.144904 nuclear receptor co-repressor 1 /FL=gb:AF044209.1 gb:NM_006311.1
206075_s_at	-1.85	gb:NM_001895.1 /DEF=Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), mRNA. /FEA=mRNA /GEN=CSNK2A1 /PROD=casein kinase 2, alpha 1 polypeptide /DB_XREF=gi:4503094 /UG=Hs.155140 casein kinase 2, alpha 1 polypeptide /FL=gb:M55265.1 gb:NM_001895.1 gb:J02853.1
215296_at	-1.85	Consensus includes gb:AK027000.1 /DEF=Homo sapiens cDNA: FLJ23347 fis, clone HEP13727. /FEA=mRNA /DB_XREF=gi:10440000 /UG=Hs.18586 KIAA0451 gene product
201860_s_at	-1.86	gb:NM_000930.1 /DEF=Homo sapiens plasminogen activator, tissue (PLAT), mRNA. /FEA=mRNA /GEN=PLAT /PROD=plasminogen activator, tissue /DB_XREF=gi:4505860 /UG=Hs.274404 plasminogen activator, tissue /FL=gb:NM_000931.1 gb:M15518.1 gb:M18182.1 gb:NM_000930.1
213056_at	-1.86	Consensus includes gb:AU145019 /FEA=EST /DB_XREF=gi:11006540 /DB_XREF=est:AU145019 /CLONE=HEMBA1003646 /UG=Hs.96427 KIAA1013 protein
219166_at	-1.87	gb:NM_018139.1 /DEF=Homo sapiens hypothetical protein FLJ10563 (FLJ10563), mRNA. /FEA=mRNA /GEN=FLJ10563 /PROD=hypothetical protein FLJ10563 /DB_XREF=gi:8922518 /UG=Hs.265960 hypothetical protein FLJ10563 /FL=gb:NM_018139.1
220559_at	-1.87	gb:NM_001426.2 /DEF=Homo sapiens engrailed homolog 1 (EN1), mRNA. /FEA=mRNA /GEN=EN1 /PROD=engrailed homolog 1 /DB_XREF=gi:7710118 /UG=Hs.271977 engrailed homolog 1 /FL=gb:NM_001426.2
208070_s_at	-1.87	gb:NM_002912.1 /DEF=Homo sapiens REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta (REV3L), mRNA. /FEA=mRNA /GEN=REV3L /PROD=REV3 (yeast homolog)-like, catalytic subunit ofDNA polymerase zeta /DB_XREF=gi:4506482 /UG=Hs.115521 REV3 (yeast homolog)-like, catalytic subunit of DNA polymerase zeta /FL=gb:AF078695.1 gb:NM_002912.1 gb:AF179428.1
213992_at	-1.87	Consensus includes gb:AI889941 /FEA=EST /DB_XREF=gi:5595105 /DB_XREF=est:wm65d06.x1 /CLONE=IMAGE:2440811 /UG=Hs.408 collagen, type IV, alpha 6
214734_at	-1.88	Consensus includes gb:AB014524.1 /DEF=Homo sapiens mRNA for KIAA0624 protein, partial cds. /FEA=mRNA /GEN=KIAA0624 /PROD=KIAA0624 protein /DB_XREF=gi:3327061 /UG=Hs.138380 KIAA0624 protein
218649_x_at	-1.88	gb:NM_004713.1 /DEF=Homo sapiens serologically defined colon cancer antigen 1 (SDCCAG1), mRNA. /FEA=mRNA /GEN=SDCCAG1 /PROD=serologically defined colon cancer antigen 1 /DB_XREF=gi:4759077 /UG=Hs.54900 serologically defined colon cancer antigen 1 /FL=gb:AF039687.1 gb:NM_004713.1
211574_s_at	-1.88	gb:D84105.1 /DEF=Human CD46 mRNA, complete cds. /FEA=mRNA /PROD=CD46 /DB_XREF=gi:1256700 /UG=Hs.83532 membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen) /FL=gb:D84105.1
218142_s_at	-1.88	gb:NM_016302.1 /DEF=Homo sapiens protein x 0001 (LOC51185), mRNA. /FEA=mRNA /GEN=LOC51185 /PROD=protein x 0001 /DB_XREF=gi:10047097 /UG=Hs.18925 protein x 0001 /FL=gb:NM_016302.1 gb:AF117230.1
219822_at	-1.88	gb:NM_004294.1 /DEF=Homo sapiens mitochondrial translational release factor 1 (MTRF1), mRNA. /FEA=mRNA /GEN=MTRF1 /PROD=mitochondrial translational release factor 1 /DB_XREF=gi:4758743 /UG=Hs.80683

		mitochondrial translational release factor 1 /FL=gb:AF072934.1 gb:NM_004294.1
206654_s_at	-1.88	gb:NM_006467.1 /DEF=Homo sapiens polymerase (RNA) III (DNA directed) (32kD) (RPC32), mRNA. /FEA=mRNA /GEN=RPC32 /PROD=polymerase (RNA) III (DNA directed) (32kD) /DB_XREF=gi:5454017 /UG=Hs.282387 polymerase (RNA) III (DNA directed) (32kD) /FL=gb:U93868.1 gb:NM_006467.1
218940_at	-1.89	gb:NM_024558.1 /DEF=Homo sapiens hypothetical protein FLJ13920 (FLJ13920), mRNA. /FEA=mRNA /GEN=FLJ13920 /PROD=hypothetical protein FLJ13920 /DB_XREF=gi:13375724 /UG=Hs.13056 hypothetical protein FLJ13920 /FL=gb:NM_024558.1
202731_at	-1.9	gb:NM_014456.1 /DEF=Homo sapiens programmed cell death 4 (PDCD4), mRNA. /FEA=mRNA /GEN=PDCD4 /PROD=programmed cell death 4 /DB_XREF=gi:7657448 /UG=Hs.296251 programmed cell death 4 /FL=gb:U96628.1 gb:NM_014456.1
203786_s_at	-1.9	gb:NM_003287.1 /DEF=Homo sapiens tumor protein D52-like 1 (TPD52L1), mRNA. /FEA=mRNA /GEN=TPD52L1 /PROD=tumor protein D52-like 1 /DB_XREF=gi:4507640 /UG=Hs.16611 tumor protein D52-like 1 /FL=gb:U44427.1 gb:NM_003287.1
205540_s_at	-1.93	gb:NM_016656.1 /DEF=Homo sapiens GTP-binding protein ragB (RAGB), transcript variant RAGBl, mRNA. /FEA=mRNA /GEN=RAGB /PROD=GTP-binding protein ragB long isoform /DB_XREF=gi:8051626 /UG=Hs.50282 GTP-binding protein ragB /FL=gb:NM_016656.1
208693_s_at	-1.94	gb:D30658.1 /DEF=Human T-cell mRNA for glycyl tRNA synthetase, complete cds. /FEA=mRNA /PROD=glycyl tRNA synthetase /DB_XREF=gi:577711 /UG=Hs.75280 glycyl-tRNA synthetase /FL=gb:D30658.1 gb:U09587.1 gb:NM_002047.1
219100_at	-1.94	gb:NM_024928.1 /DEF=Homo sapiens hypothetical protein FLJ22559 (FLJ22559), mRNA. /FEA=mRNA /GEN=FLJ22559 /PROD=hypothetical protein FLJ22559 /DB_XREF=gi:13487922 /UG=Hs.273387 hypothetical protein FLJ22559 /FL=gb:NM_024928.1
218138_at	-1.95	gb:NM_018848.1 /DEF=Homo sapiens McKusick-Kaufman syndrome (MKKS), mRNA. /FEA=mRNA /GEN=MKKS /PROD=McKusick-Kaufman syndrome protein /DB_XREF=gi:9055271 /UG=Hs.46743 McKusick-Kaufman syndrome /FL=gb:AF275813.1 gb:AF221992.1 gb:AF221993.1 gb:NM_018848.1
202402_s_at	-1.95	gb:NM_001751.1 /DEF=Homo sapiens cysteinyl-tRNA synthetase (CARS), mRNA. /FEA=mRNA /GEN=CARS /PROD=cysteinyl-tRNA synthetase /DB_XREF=gi:10835050 /UG=Hs.159604 cysteinyl-tRNA synthetase /FL=gb:NM_001751.1 gb:BC002880.1 gb:AF288206.1 gb:AF288207.1
200769_s_at	-1.96	gb:NM_005911.1 /DEF=Homo sapiens methionine adenosyltransferase II, alpha (MAT2A), mRNA. /FEA=mRNA /GEN=MAT2A /PROD=methionine adenosyltransferase II, alpha /DB_XREF=gi:5174528 /UG=Hs.77502 methionine adenosyltransferase II, alpha /FL=gb:BC001686.1 gb:BC001854.1 gb:NM_005911.1
212325_at	-1.97	Consensus includes gb:AK027231.1 /DEF=Homo sapiens cDNA: FLJ23578 fis, clone LNG12709. /FEA=mRNA /DB_XREF=gi:10440313 /UG=Hs.202949 KIAA1102 protein
222282_at	-1.97	Consensus includes gb:AV761453 /FEA=EST /DB_XREF=gi:10919301 /DB_XREF=est:AV761453 /CLONE=MDSBZA03 /UG=Hs.294014 ESTs
203223_at	-1.97	gb:NM_004703.1 /DEF=Homo sapiens rabaptin-5 (RAB5EP), mRNA. /FEA=mRNA /GEN=RAB5EP /PROD=rabaptin-5 /DB_XREF=gi:4759005 /UG=Hs.326056 rabaptin-5 /FL=gb:NM_004703.1
208933_s_at	-1.98	Consensus includes gb:AI659005 /FEA=EST /DB_XREF=gi:4762575 /DB_XREF=est:tu23e02.x1 /CLONE=IMAGE:2251898 /UG=Hs.4082 lectin, galactoside-binding, soluble, 8 (galectin 8) /FL=gb:AF342815.1 gb:L78132.1 gb:AF074000.1 gb:NM_006499.1
218276_s_at	-1.98	gb:NM_021818.1 /DEF=Homo sapiens WW Domain-Containing Gene (WW45), mRNA. /FEA=mRNA /GEN=WW45 /PROD=WW Domain-Containing Gene /DB_XREF=gi:11141888 /UG=Hs.288906 WW Domain-Containing Gene /FL=gb:NM_021818.1

215012_at	-1.98	Consensus includes gb:AU144775 /FEA=EST /DB_XREF=gi:11006296 /DB_XREF=est:AU144775 /CLONE=HEMBA1002935 /UG=Hs.172329 KIAA0576 protein
203459_s_at	-1.98	gb:NM_022575.1 /DEF=Homo sapiens vacuolar protein sorting 16 (yeast homolog) (VPS16), mRNA. /FEA=mRNA /GEN=VPS16 /PROD=vacuolar protein sorting 16 (yeast homolog) /DB_XREF=gi:12007657 /UG=Hs.302441 vacuolar protein sorting 16 (yeast homolog) /FL=gb:AF308801.1 gb:NM_022575.1
221771_s_at	-1.98	Consensus includes gb:BC003542.1 /DEF=Homo sapiens, clone IMAGE:3611719, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3611719) /DB_XREF=gi:13097656 /UG=Hs.244482 Homo sapiens, clone IMAGE:3611719, mRNA, partial cds
207564_x_at	-1.98	gb:NM_003605.2 /DEF=Homo sapiens O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA. /FEA=mRNA /GEN=OGT /PROD=O-linked GlcNAc transferase /DB_XREF=gi:6006036 /UG=Hs.100293 O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) /FL=gb:U77413.1 gb:NM_003605.2
205063_at	-1.98	gb:NM_003616.1 /DEF=Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1), mRNA. /FEA=mRNA /GEN=SIP1 /PROD=survival of motor neuron protein interactingprotein 1 /DB_XREF=gi:4506960 /UG=Hs.102456 survival of motor neuron protein interacting protein 1 /FL=gb:AF027150.1 gb:NM_003616.1
217776_at	-1.99	gb:AF167438.1 /DEF=Homo sapiens androgen-regulated short-chain dehydrogenasereductase 1 (ARSDR1) mRNA, complete cds. /FEA=mRNA /GEN=ARSDR1 /PROD=androgen-regulated short-chaindehydrogenasereductase 1 /DB_XREF=gi:9622123 /UG=Hs.179817 CGI-82 protein /FL=gb:BC000112.1 gb:AF151840.1 gb:NM_016026.1 gb:AF167438.1
202458_at	-1.99	gb:NM_007173.1 /DEF=Homo sapiens protease, serine, 23 (SPUVE), mRNA. /FEA=mRNA /GEN=SPUVE /PROD=protease, serine, 23 /DB_XREF=gi:6005881 /UG=Hs.325820 protease, serine, 23 /FL=gb:AL136914.1 gb:BC001278.1 gb:AF015287.1 gb:NM_007173.1 gb:AF193611.1
220173_at	-1.99	gb:NM_025057.1 /DEF=Homo sapiens hypothetical protein FLJ23189 (FLJ23189), mRNA. /FEA=mRNA /GEN=FLJ23189 /PROD=hypothetical protein FLJ23189 /DB_XREF=gi:13376590 /UG=Hs.287733 hypothetical protein FLJ23189 /FL=gb:NM_025057.1
212328_at	-2	Consensus includes gb:AB029025.1 /DEF=Homo sapiens mRNA for KIAA1102 protein, partial cds. /FEA=mRNA /GEN=KIAA1102 /PROD=KIAA1102 protein /DB_XREF=gi:5689540 /UG=Hs.202949 KIAA1102 protein
218251_at	-2	gb:NM_021242.1 /DEF=Homo sapiens hypothetical protein STRAIT11499 (STRAIT11499), mRNA. /FEA=mRNA /GEN=STRAIT11499 /PROD=hypothetical protein STRAIT11499 /DB_XREF=gi:10864050 /UG=Hs.236556 hypothetical protein STRAIT11499 /FL=gb:NM_021242.1
203787_at	-2.01	gb:NM_012446.1 /DEF=Homo sapiens single-stranded-DNA-binding protein (SSBP2), mRNA. /FEA=mRNA /GEN=SSBP2 /PROD=single-stranded-DNA-binding protein /DB_XREF=gi:7106422 /UG=Hs.169833 single-stranded-DNA-binding protein /FL=gb:AL080076.1 gb:AF161465.1 gb:NM_012446.1
211657_at	-2.01	gb:M18728.1 /DEF=Human nonspecific crossreacting antigen mRNA, complete cds. /FEA=mRNA /GEN=NCA; NCA; NCA /PROD=non-specific cross reacting antigen /DB_XREF=gi:189084 /FL=gb:M18728.1
204681_s_at	-2.01	gb:NM_012294.1 /DEF=Homo sapiens guanine nucleotide exchange factor for Rap1; M-Ras-regulated GEF (KIAA0277), mRNA. /FEA=mRNA /GEN=KIAA0277 /PROD=guanine nucleotide exchange factor for Rap1;M-Ras-regulated GEF /DB_XREF=gi:6912455 /UG=Hs.80620 guanine nucleotide exchange factor for Rap1; M-Ras-regulated GEF /FL=gb:D87467.1 gb:NM_012294.1
202430_s_at	-2.01	gb:NM_021105.1 /DEF=Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA. /FEA=mRNA /GEN=PLSCR1 /PROD=phospholipid scramblase 1 /DB_XREF=gi:10863876 /UG=Hs.198282 phospholipid scramblase 1 /FL=gb:NM_021105.1 gb:AB006746.1 gb:AF098642.1

217653_x_at	-2.02	Consensus includes gb:AW150065 /FEA=EST /DB_XREF=gi:6197971 /DB_XREF=est:xg48a10.x1 /CLONE=IMAGE:2630778 /UG=Hs.271957 ESTs
217738_at	-2.02	Consensus includes gb:BF575514 /FEA=EST /DB_XREF=gi:11649318 /DB_XREF=est:602133090F1 /CLONE=IMAGE:4288079 /UG=Hs.239138 pre-B-cell colony-enhancing factor /FL=gb:U02020.1 gb:NM_005746.1
218006_s_at	-2.02	gb:NM_006963.1 /DEF=Homo sapiens zinc finger protein 22 (KOX 15) (ZNF22), mRNA. /FEA=mRNA /GEN=ZNF22 /PROD=zinc finger protein 22 (KOX 15) /DB_XREF=gi:5902159 /UG=Hs.108642 zinc finger protein 22 (KOX 15) /FL=gb:NM_006963.1
217906_at	-2.02	gb:NM_014315.1 /DEF=Homo sapiens host cell factor homolog (LCP), mRNA. /FEA=mRNA /GEN=LCP /PROD=host cell factor homolog /DB_XREF=gi:7657300 /UG=Hs.20597 host cell factor homolog /FL=gb:BC002335.1 gb:AF113131.1 gb:NM_014315.1 gb:AF244137.1
217807_s_at	-2.02	gb:NM_015710.1 /DEF=Homo sapiens glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA. /FEA=mRNA /GEN=GLTSCR2 /PROD=glioma tumor suppressor candidate region gene 2 /DB_XREF=gi:7657129 /UG=Hs.2237 glioma tumor suppressor candidate region gene 2 /FL=gb:AF182076.1 gb:NM_015710.1
214012_at	-2.02	Consensus includes gb:BE551138 /FEA=EST /DB_XREF=gi:9792830 /DB_XREF=est:7b55a07.x1 /CLONE=IMAGE:3232116 /UG=Hs.247043 type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
201816_s_at	-2.03	gb:NM_001483.1 /DEF=Homo sapiens glioblastoma amplified sequence (GBAS), mRNA. /FEA=mRNA /GEN=GBAS /PROD=glioblastoma amplified sequence /DB_XREF=gi:4503936 /UG=Hs.152707 glioblastoma amplified sequence /FL=gb:BC000732.1 gb:BC001837.1 gb:AF029786.1 gb:NM_001483.1
213703_at	-2.04	Consensus includes gb:W95043 /FEA=EST /DB_XREF=gi:1424182 /DB_XREF=est:zh46c11.s1 /CLONE=IMAGE:415124 /UG=Hs.79732 fibulin 1
219754_at	-2.04	gb:NM_018301.1 /DEF=Homo sapiens hypothetical protein FLJ11016 (FLJ11016), mRNA. /FEA=mRNA /GEN=FLJ11016 /PROD=hypothetical protein FLJ11016 /DB_XREF=gi:8922825 /UG=Hs.210859 hypothetical protein FLJ11016 /FL=gb:NM_018301.1
220773_s_at	-2.05	gb:NM_020806.1 /DEF=Homo sapiens gephyrin (GPH), mRNA. /FEA=mRNA /GEN=GPH /PROD=gephryin /DB_XREF=gi:10880982 /UG=Hs.13405 gephyrin /FL=gb:NM_020806.1
213122_at	-2.05	Consensus includes gb:AI096375 /FEA=EST /DB_XREF=gi:3446286 /DB_XREF=est:qb91e08.x1 /CLONE=IMAGE:1707494 /UG=Hs.173094 Homo sapiens mRNA for KIAA1750 protein, partial cds
201415_at	-2.05	gb:NM_000178.1 /DEF=Homo sapiens glutathione synthetase (GSS), mRNA. /FEA=mRNA /GEN=GSS /PROD=glutathione synthetase /DB_XREF=gi:4504168 /UG=Hs.82327 glutathione synthetase /FL=gb:U34683.1 gb:NM_000178.1
210372_s_at	-2.05	gb:AF208012.1 /DEF=Homo sapiens tumor protein D52-like 2 (TPD52L2) mRNA, complete cds. /FEA=mRNA /GEN=TPD52L2 /PROD=tumor protein D52-like 2 /DB_XREF=gi:12246900 /UG=Hs.16611 tumor protein D52-like 1 /FL=gb:AF208012.1
204278_s_at	-2.05	gb:NM_004215.1 /DEF=Homo sapiens estrogen receptor binding site associated, antigen, 9 (EBAG9), mRNA. /FEA=mRNA /GEN=EBAG9 /PROD=estrogen receptor binding site associated,antigen, 9 /DB_XREF=gi:4758229 /UG=Hs.9222 estrogen receptor binding site associated, antigen, 9 /FL=gb:BC005249.1 gb:AF006265.1 gb:AB007619.1 gb:NM_004215.1
213737_x_at	-2.05	Consensus includes gb:AI620911 /FEA=EST /DB_XREF=gi:4630037 /DB_XREF=est:tu05d12.x1 /CLONE=IMAGE:2250167 /UG=Hs.205125 ESTs
210425_x_at	-2.05	gb:AF164622.1 /DEF=Homo sapiens golgin-67 (GOLGA5) mRNA, complete cds. /FEA=mRNA /GEN=GOLGA5 /PROD=golgin-67 /DB_XREF=gi:7211437 /UG=Hs.182982 golgin-67 /FL=gb:AF163441.1 gb:AF164622.1
205531_s_at	-2.06	gb:NM_013267.1 /DEF=Homo sapiens breast cell glutaminase (GA), mRNA. /FEA=mRNA /GEN=GA

		/PROD=breast cell glutaminase /DB_XREF=gi:7019388 /UG=Hs.325443 breast cell glutaminase /FL=gb:AF110330.1 gb:AF110331.1 gb:AF223944.1 gb:NM_013267.1
217941_s_at	-2.06	gb:NM_018695.1 /DEF=Homo sapiens erbb2-interacting protein ERBIN (LOC55914), mRNA. /FEA=mRNA /GEN=LOC55914 /PROD=erbb2-interacting protein ERBIN /DB_XREF=gi:8923908 /UG=Hs.8117 erbb2-interacting protein ERBIN /FL=gb:AF263744.1 gb:NM_018695.1
213283_s_at	-2.06	Consensus includes gb:BG285616 /FEA=EST /DB_XREF=gi:13037752 /DB_XREF=est:602380622F1 /CLONE=IMAGE:4498325 /UG=Hs.79971 sal (Drosophila)-like 2
205173_x_at	-2.06	gb:NM_001779.1 /DEF=Homo sapiens CD58 antigen, (lymphocyte function-associated antigen 3) (CD58), mRNA. /FEA=mRNA /GEN=CD58 /PROD=CD58 antigen, (lymphocyte function-associatedantigen 3) /DB_XREF=gi:4502676 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3) /FL=gb:NM_001779.1
214212_x_at	-2.06	Consensus includes gb:AI928241 /FEA=EST /DB_XREF=gi:5664205 /DB_XREF=est:wo95g11.x1 /CLONE=IMAGE:2463140 /UG=Hs.75260 mitogen inducible 2
221081_s_at	-2.06	gb:NM_024901.1 /DEF=Homo sapiens hypothetical protein FLJ22457 (FLJ22457), mRNA. /FEA=mRNA /GEN=FLJ22457 /PROD=hypothetical protein FLJ22457 /DB_XREF=gi:13376358 /UG=Hs.238707 hypothetical protein FLJ22457 /FL=gb:NM_024901.1
219767_s_at	-2.07	gb:NM_005111.1 /DEF=Homo sapiens crystallin, zeta (quinone reductase)-like 1 (CRYZL1), mRNA. /FEA=mRNA /GEN=CRYZL1 /PROD=crystallin, zeta (quinone reductase)-like 1 /DB_XREF=gi:4826679 /UG=Hs.330208 crystallin, zeta (quinone reductase)-like 1 /FL=gb:AF029689.1 gb:NM_005111.1
219513_s_at	-2.07	gb:NM_005490.1 /DEF=Homo sapiens novel SH2-containing protein 1 (NSP1), mRNA. /FEA=mRNA /GEN=NSP1 /PROD=novel SH2-containing protein 1 /DB_XREF=gi:4885524 /UG=Hs.268541 novel SH2-containing protein 1 /FL=gb:AF124249.1 gb:NM_005490.1
218637_at	-2.07	gb:NM_018439.1 /DEF=Homo sapiens hypothetical protein IMPACT (IMPACT), mRNA. /FEA=mRNA /GEN=IMPACT /PROD=hypothetical protein IMPACT /DB_XREF=gi:8923818 /UG=Hs.284245 hypothetical protein IMPACT /FL=gb:AF208694.1 gb:AB026264.1 gb:NM_018439.1
215208_x_at	-2.08	Consensus includes gb:AK021571.1 /DEF=Homo sapiens cDNA FLJ11509 fis, clone HEMBA1002166. /FEA=mRNA /DB_XREF=gi:10432777 /UG=Hs.289093 Homo sapiens cDNA FLJ11509 fis, clone HEMBA1002166
212177_at	-2.08	Consensus includes gb:AW081113 /FEA=EST /DB_XREF=gi:6036265 /DB_XREF=est:xc29c08.x1 /CLONE=IMAGE:2585678 /UG=Hs.18368 DKFZP564B0769 protein
201685_s_at	-2.08	gb:NM_014828.1 /DEF=Homo sapiens KIAA0737 gene product (KIAA0737), mRNA. /FEA=mRNA /GEN=KIAA0737 /PROD=KIAA0737 gene product /DB_XREF=gi:7662273 /UG=Hs.194035 KIAA0737 gene product /FL=gb:AB018280.1 gb:NM_014828.1
212971_at	-2.09	Consensus includes gb:AI769685 /FEA=EST /DB_XREF=gi:5236194 /DB_XREF=est:wj25f08.x1 /CLONE=IMAGE:2403879 /UG=Hs.159604 cysteinyl-tRNA synthetase
218204_s_at	-2.09	gb:NM_024513.1 /DEF=Homo sapiens FYVE and coiled-coil domain containing 1 (FYCO1), mRNA. /FEA=mRNA /GEN=FYCO1 /PROD=FYVE and coiled-coil domain containing 1 /DB_XREF=gi:13470091 /UG=Hs.257267 FYVE and coiled-coil domain containing 1 /FL=gb:NM_024513.1
202990_at	-2.09	gb:NM_002863.1 /DEF=Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA. /FEA=mRNA /GEN=PYGL /PROD=phosphorylase, glycogen; liver (Hers disease,glycogen storage disease type VI) /DB_XREF=gi:4506352 /UG=Hs.771 phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) /FL=gb:M14636.1 gb:AF066858.1 gb:AF046785.1 gb:NM_002863.1
202536_at	-2.09	Consensus includes gb:AK002165.1 /DEF=Homo sapiens cDNA FLJ11303 fis, clone PLACE1009995, highly

		similar to Homo sapiens mRNA; cDNA DKFZp564O123. /FEA=mRNA /DB_XREF=gi:7023876 /UG=Hs.11449 DKFZP564O123 protein /FL=gb:AF151842.1 gb:AL080122.1 gb:NM_014043.1
209481_at	-2.09	gb:AF226044.1 /DEF=Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds. /FEA=mRNA /GEN=HSNFRK /PROD=HSNFRK /DB_XREF=gi:9295326 /UG=Hs.79025 KIAA0096 protein /FL=gb:AF226044.1
206059_at	-2.1	gb:NM_003430.1 /DEF=Homo sapiens zinc finger protein 91 (HPF7, HTF10) (ZNF91), mRNA. /FEA=mRNA /GEN=ZNF91 /PROD=zinc finger protein 91 (HPF7, HTF10) /DB_XREF=gi:4508040 /UG=Hs.8597 zinc finger protein 91 (HPF7, HTF10) /FL=gb:L11672.1 gb:NM_003430.1
209610_s_at	-2.1	Consensus includes gb:BF340083 /FEA=EST /DB_XREF=gi:11286545 /DB_XREF=est:602037236F1 /CLONE=IMAGE:4185248 /UG=Hs.323878 solute carrier family 1 (glutamateneutral amino acid transporter), member 4 /FL=gb:L14595.1 gb:NM_003038.1 gb:L19444.1 gb:AB026689.1
218323_at	-2.1	gb:NM_018307.1 /DEF=Homo sapiens hypothetical protein FLJ11040 (FLJ11040), mRNA. /FEA=mRNA /GEN=FLJ11040 /PROD=hypothetical protein FLJ11040 /DB_XREF=gi:8922837 /UG=Hs.14202 hypothetical protein FLJ11040 /FL=gb:NM_018307.1
207231_at	-2.1	gb:NM_014648.1 /DEF=Homo sapiens KIAA0675 gene product (KIAA0675), mRNA. /FEA=mRNA /GEN=KIAA0675 /PROD=KIAA0675 gene product /DB_XREF=gi:7662243 /UG=Hs.165662 KIAA0675 gene product /FL=gb:AB014575.1 gb:NM_014648.1
203140_at	-2.11	gb:NM_001706.1 /DEF=Homo sapiens B-cell CLLlymphoma 6 (zinc finger protein 51) (BCL6), mRNA. /FEA=mRNA /GEN=BCL6 /PROD=B-cell CLLlymphoma 6 (zinc finger protein 51) /DB_XREF=gi:4502382 /UG=Hs.155024 B-cell CLLlymphoma 6 (zinc finger protein 51) /FL=gb:U00115.1 gb:NM_001706.1
209098_s_at	-2.11	gb:U61276.1 /DEF=Human transmembrane protein Jagged 1 (HJ1) mRNA, complete cds. /FEA=mRNA /GEN=HJ1 /PROD=transmembrane protein Jagged 1 /DB_XREF=gi:1438936 /UG=Hs.91143 jagged 1 (Alagille syndrome) /FL=gb:U61276.1 gb:U73936.1 gb:AF003837.1 gb:AF028593.1 gb:NM_000214.1
218924_s_at	-2.11	gb:NM_004388.1 /DEF=Homo sapiens chitobiase, di-N-acetyl- (CTBS), mRNA. /FEA=mRNA /GEN=CTBS /PROD=chitobiase, di-N-acetyl- /DB_XREF=gi:4758091 /UG=Hs.135578 chitobiase, di-N-acetyl- /FL=gb:M95767.1 gb:NM_004388.1
203762_s_at	-2.12	gb:NM_016008.1 /DEF=Homo sapiens CGI-60 protein (LOC51626), mRNA. /FEA=mRNA /GEN=LOC51626 /PROD=CGI-60 protein /DB_XREF=gi:7706299 /UG=Hs.7627 CGI-60 protein /FL=gb:AF151818.1 gb:NM_016008.1
212675_s_at	-2.12	Consensus includes gb:AB011154.1 /DEF=Homo sapiens mRNA for KIAA0582 protein, partial cds. /FEA=mRNA /GEN=KIAA0582 /PROD=KIAA0582 protein /DB_XREF=gi:3043687 /UG=Hs.79507 KIAA0582 protein
203552_at	-2.12	Consensus includes gb:AW298170 /FEA=EST /DB_XREF=gi:6704806 /DB_XREF=est:UI-H-BW0-ajt-a-06-0-UI.s1 /CLONE=IMAGE:2732819 /UG=Hs.246970 mitogen-activated protein kinase kinase kinase kinase 5 /FL=gb:U77129.1 gb:NM_006575.1
212072_s_at	-2.12	Consensus includes gb:AL049761 /DEF=Human DNA sequence from clone RP5-863C7 on chromosome 20p12.3-13. Contains the CSNK2A1 gene for casein kinase 2 alpha 1 polypeptide (EC 2.7.1.37), ESTs, STSs and GSSs /FEA=mRNA_2 /DB_XREF=gi:5738437 /UG=Hs.155140 casein kinase 2, alpha 1 polypeptide
211776_s_at	-2.13	gb:BC006141.1 /DEF=Homo sapiens, Similar to erythrocyte protein band 4.1-like 3, clone MGC:13087, mRNA, complete cds. /FEA=mRNA /PROD=Similar to erythrocyte protein band 4.1-like 3 /DB_XREF=gi:13544008 /FL=gb:BC006141.1
211744_s_at	-2.13	gb:BC005930.1 /DEF=Homo sapiens, Similar to CD58 antigen, (lymphocyte function-associated antigen 3), clone MGC:14538, mRNA, complete cds. /FEA=mRNA /PROD=Similar to CD58 antigen, (lymphocytefunction-associated antigen 3) /DB_XREF=gi:13543544 /FL=gb:BC005930.1
214544_s_at	-2.13	Consensus includes gb:NM_003825.1 /DEF=Homo sapiens synaptosomal-associated protein, 23kD (SNAP23),

		mRNA. /FEA=CDS /GEN=SNAP23 /PROD=synaptosomal-associated protein, 23kD /DB_XREF=gi:4507096 /UG=Hs.184376 synaptosomal-associated protein, 23kD /FL=gb:Y09568.1 gb:NM_003825.1
219276_x_at	-2.13	gb:NM_024828.1 /DEF=Homo sapiens hypothetical protein FLJ13657 (FLJ13657), mRNA. /FEA=mRNA /GEN=FLJ13657 /PROD=hypothetical protein FLJ13657 /DB_XREF=gi:13376229 /UG=Hs.178357 hypothetical protein FLJ13657 /FL=gb:NM_024828.1
201810_s_at	-2.13	Consensus includes gb:AL562152 /FEA=EST /DB_XREF=gi:12910291 /DB_XREF=est:AL562152 /CLONE=CS0DC001YK23 (3 prime) /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1
209311_at	-2.13	gb:D87461.1 /DEF=Human mRNA for KIAA0271 gene, complete cds. /FEA=mRNA /GEN=KIAA0271 /DB_XREF=gi:1944417 /UG=Hs.75244 BCL2-like 2 /FL=gb:U59747.1 gb:D87461.1 gb:NM_004050.1
60794_f_at	-2.13	Cluster Incl. AI400621:tg49g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2112146 /clone_end=3 /gb=AI400621 /gi=4243708 /ug=Hs.213640 /len=529
203757_s_at	-2.13	gb:BC005008.1 /DEF=Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds. /FEA=mRNA /PROD=carcinoembryonic antigen-related cell adhesionmolecule 6 (non-specific cross reacting antigen) /DB_XREF=gi:13477106 /UG=Hs.73848 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) /FL=gb:BC005008.1 gb:M18216.1 gb:M29541.1 gb:NM_002483.1
215304_at	-2.14	Consensus includes gb:U79293.1 /DEF=Human clone 23948 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710274 /UG=Hs.159264 Human clone 23948 mRNA sequence
201941_at	-2.14	Consensus includes gb:BE349147 /FEA=EST /DB_XREF=gi:9261086 /DB_XREF=est:ht51f05.x1 /CLONE=IMAGE:3150273 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:D85390.1 gb:NM_001304.2
215079_at	-2.15	Consensus includes gb:AK026723.1 /DEF=Homo sapiens cDNA: FLJ23070 fis, clone LNG05629. /FEA=mRNA /DB_XREF=gi:10439641 /UG=Hs.30579 Homo sapiens cDNA: FLJ23070 fis, clone LNG05629
205891_at	-2.15	gb:NM_000676.1 /DEF=Homo sapiens adenosine A2b receptor (ADORA2B), mRNA. /FEA=mRNA /GEN=ADORA2B /PROD=adenosine A2b receptor /DB_XREF=gi:4501950 /UG=Hs.45743 adenosine A2b receptor /FL=gb:M97759.1 gb:NM_000676.1
207267_s_at	-2.16	gb:NM_018962.1 /DEF=Homo sapiens Down syndrome critical region gene 6 (DSCR6), mRNA. /FEA=mRNA /GEN=DSCR6 /PROD=Down syndrome critical region protein 6 /DB_XREF=gi:9506556 /UG=Hs.254560 Down syndrome critical region gene 6 /FL=gb:AB037158.1 gb:NM_018962.1
203355_s_at	-2.16	gb:NM_015310.1 /DEF=Homo sapiens KIAA0942 protein (KIAA0942), mRNA. /FEA=mRNA /GEN=KIAA0942 /PROD=KIAA0942 protein /DB_XREF=gi:7662395 /UG=Hs.6763 KIAA0942 protein /FL=gb:AF243495.2 gb:NM_015310.1
203553_s_at	-2.16	gb:NM_006575.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase kinase 5 (MAP4K5), mRNA. /FEA=mRNA /GEN=MAP4K5 /PROD=mitogen-activated protein kinase kinase kinasekinase /DB_XREF=gi:5729890 /UG=Hs.246970 mitogen-activated protein kinase kinase kinase kinase 5 /FL=gb:U77129.1 gb:NM_006575.1
216858_x_at	-2.16	Consensus includes gb:AL080112.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586H0722 (from clone DKFZp586H0722). /FEA=mRNA /DB_XREF=gi:5262539 /UG=Hs.332731 Homo sapiens mRNA; cDNA DKFZp586H0722 (from clone DKFZp586H0722)
218307_at	-2.16	gb:NM_018346.1 /DEF=Homo sapiens hypothetical protein FLJ11164 (FLJ11164), mRNA. /FEA=mRNA /GEN=FLJ11164 /PROD=hypothetical protein FLJ11164 /DB_XREF=gi:8922910 /UG=Hs.8033 hypothetical protein FLJ11164 /FL=gb:NM_018346.1
204350_s_at	-2.17	gb:NM_004270.1 /DEF=Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9 (33kD)

		(CRSP9), mRNA. /FEA=mRNA /GEN=CRSP9 /PROD=cofactor required for Sp1 transcriptionalactivation, subunit 9 (33kD) /DB_XREF=gi:4758063 /UG=Hs.279902 cofactor required for Sp1 transcriptional activation, subunit 9 (33kD) /FL=gb:BC005250.1 gb:AF031383.1 gb:AF104251.1 gb:NM_004270.1
213273_at	-2.17	Consensus includes gb:BF112171 /FEA=EST /DB_XREF=gi:10941861 /DB_XREF=est:7l48d06.x1 /CLONE=IMAGE:3524770 /UG=Hs.5028 DKFZP564O0423 protein
212634_at	-2.17	Consensus includes gb:AW298092 /FEA=EST /DB_XREF=gi:6704728 /DB_XREF=est:UI-H-BW0-ajs-b-03-0-UI.s1 /CLONE=IMAGE:2732860 /UG=Hs.5460 KIAA0776 protein
219973_at	-2.17	gb:NM_024590.1 /DEF=Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /FEA=mRNA /GEN=FLJ23548 /PROD=hypothetical protein FLJ23548 /DB_XREF=gi:13375780 /UG=Hs.22895 hypothetical protein FLJ23548 /FL=gb:NM_024590.1
212183_at	-2.18	Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149213 /DB_XREF=est:hd43g08.x1 /CLONE=IMAGE:2912318 /UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type motif 4
203765_at	-2.18	gb:NM_012198.1 /DEF=Homo sapiens grancalcin (GCL), mRNA. /FEA=mRNA /GEN=GCL /PROD=grancalcin /DB_XREF=gi:6912387 /UG=Hs.79381 grancalcin /FL=gb:BC005214.1 gb:M81637.1 gb:NM_012198.1
217988_at	-2.18	gb:NM_021178.1 /DEF=Homo sapiens enhancer of invasion 10 (HEI10), mRNA. /FEA=mRNA /GEN=HEI10 /PROD=enhancer of invasion 10 /DB_XREF=gi:10863978 /UG=Hs.107003 enhancer of invasion 10 /FL=gb:NM_021178.1 gb:BC000369.1 gb:BC001218.1 gb:BC004435.1 gb:AF216381.1
204682_at	-2.18	gb:NM_000428.1 /DEF=Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA. /FEA=mRNA /GEN=LTBP2 /PROD=latent transforming growth factor beta bindingprotein 2 /DB_XREF=gi:4557732 /UG=Hs.83337 latent transforming growth factor beta binding protein 2 /FL=gb:NM_000428.1
209442_x_at	-2.19	gb:AL136710.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566P0524 (from clone DKFZp566P0524); complete cds. /FEA=mRNA /GEN=DKFZp566P0524 /PROD=hypothetical protein /DB_XREF=gi:12052939 /UG=Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) /FL=gb:AL136710.1
221729_at	-2.19	Consensus includes gb:AL575735 /FEA=EST /DB_XREF=gi:12937190 /DB_XREF=est:AL575735 /CLONE=CS0DI070YK23 (3 prime) /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393.1
203538_at	-2.19	gb:NM_001745.1 /DEF=Homo sapiens calcium modulating ligand (CAMLG), mRNA. /FEA=mRNA /GEN=CAMLG /PROD=calcium modulating ligand /DB_XREF=gi:4502558 /UG=Hs.13572 calcium modulating ligand /FL=gb:NM_001745.1 gb:U18242.1
220266_s_at	-2.19	gb:NM_004235.1 /DEF=Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA. /FEA=mRNA /GEN=KLF4 /PROD=Kruppel-like factor 4 (gut) /DB_XREF=gi:4758321 /UG=Hs.7934 Kruppel-like factor 4 (gut) /FL=gb:U70663.1 gb:AF022184.1 gb:NM_004235.1 gb:AF105036.1
212976_at	-2.19	Consensus includes gb:R41498 /FEA=EST /DB_XREF=gi:816800 /DB_XREF=est:yf86h08.s1 /CLONE=IMAGE:29486 /UG=Hs.199243 KIAA0231 protein
213929_at	-2.19	Consensus includes gb:AL050204.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223). /FEA=mRNA /DB_XREF=gi:4884443 /UG=Hs.28540 Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223)
218446_s_at	-2.2	gb:NM_016078.1 /DEF=Homo sapiens CGI-148 protein (LOC51030), mRNA. /FEA=mRNA /GEN=LOC51030 /PROD=CGI-148 protein /DB_XREF=gi:7705643 /UG=Hs.6776 CGI-148 protein /FL=gb:AF151906.1 gb:AF223467.1 gb:NM_016078.1
209004_s_at	-2.2	gb:AF142481.1 /DEF=Homo sapiens F-box protein FLR1 (FLR1) mRNA, complete cds. /FEA=mRNA /GEN=FLR1 /PROD=F-box protein FLR1 /DB_XREF=gi:7672733 /UG=Hs.5548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1
206652_at	-2.2	gb:NM_016384.1 /DEF=Homo sapiens hypothetical protein (HSPC050), mRNA. /FEA=mRNA /GEN=HSPC050

		/PROD=hypothetical protein /DB_XREF=gi:7705438 /UG=Hs.278985 hypothetical protein /FL=gb:AF161535.1 gb:NM_016384.1
217106_x_at	-2.21	Consensus includes gb:AF091078.1 /DEF=Homo sapiens clone 559 unknown mRNA, complete sequence. /FEA=mRNA /PROD=unknown /DB_XREF=gi:3859993 /UG=Hs.125819 putative dimethyladenosine transferase
213995_at	-2.21	Consensus includes gb:AW195882 /FEA=EST /DB_XREF=gi:6475112 /DB_XREF=est:xn86c10.x1 /CLONE=IMAGE:2701362 /UG=Hs.56155 hypothetical protein
201761_at	-2.21	gb:NM_006636.2 /DEF=Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MTHFD2 /PROD=methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate cyclohydrolase,precursor /DB_XREF=gi:13699869 /UG=Hs.154672 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase /FL=gb:NM_006636.2
204388_s_at	-2.21	gb:NM_000240.1 /DEF=Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MAOA /PROD=monoamine oxidase A /DB_XREF=gi:4557734 /UG=Hs.183109 monoamine oxidase A /FL=gb:M68840.1 gb:M69226.1 gb:NM_000240.1
216028_at	-2.21	Consensus includes gb:AL049980.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564C152 (from clone DKFZp564C152). /FEA=mRNA /GEN=DKFZp564C152 /PROD=hypothetical protein /DB_XREF=gi:4884230 /UG=Hs.184216 DKFZP564C152 protein
217999_s_at	-2.21	Consensus includes gb:NM_007350.1 /DEF=Homo sapiens pleckstrin homology-like domain, family A, member 1 (PHLDA1), mRNA. /FEA=mRNA /GEN=PHLDA1 /PROD=pleckstrin homology-like domain, family A,member 1 /DB_XREF=gi:6679302 /UG=Hs.82101 pleckstrin homology-like domain, family A, member 1 /FL=gb:NM_007350.1
219572_at	-2.22	gb:NM_017954.1 /DEF=Homo sapiens hypothetical protein FLJ20761 (FLJ20761), mRNA. /FEA=mRNA /GEN=FLJ20761 /PROD=hypothetical protein FLJ20761 /DB_XREF=gi:8923671 /UG=Hs.107872 hypothetical protein FLJ20761 /FL=gb:NM_017954.1
203565_s_at	-2.22	gb:NM_002431.1 /DEF=Homo sapiens menage a trois 1 (CAK assembly factor) (MNAT1), mRNA. /FEA=mRNA /GEN=MNAT1 /PROD=menage a trois 1 (CAK assembly factor) /DB_XREF=gi:4505224 /UG=Hs.82380 menage a trois 1 (CAK assembly factor) /FL=gb:BC000820.1 gb:NM_002431.1
218789_s_at	-2.22	gb:NM_019021.1 /DEF=Homo sapiens hypothetical protein (FLJ20010), mRNA. /FEA=mRNA /GEN=FLJ20010 /PROD=hypothetical protein /DB_XREF=gi:9506646 /UG=Hs.91816 hypothetical protein /FL=gb:NM_019021.1
204791_at	-2.22	gb:NM_003297.1 /DEF=Homo sapiens nuclear receptor subfamily 2, group C, member 1 (NR2C1), mRNA. /FEA=mRNA /GEN=NR2C1 /PROD=nuclear receptor subfamily 2, group C, member 1 /DB_XREF=gi:4507672 /UG=Hs.108301 nuclear receptor subfamily 2, group C, member 1 /FL=gb:M29960.1 gb:NM_003297.1
218859_s_at	-2.22	gb:NM_016649.1 /DEF=Homo sapiens HDCMC28P protein (HDCMC28P), mRNA. /FEA=mRNA /GEN=HDCMC28P /PROD=HDCMC28P protein /DB_XREF=gi:7705402 /UG=Hs.88820 HDCMC28P protein /FL=gb:AF068285.1 gb:NM_016649.1
218352_at	-2.22	gb:NM_018191.1 /DEF=Homo sapiens hypothetical protein FLJ10716 (FLJ10716), mRNA. /FEA=mRNA /GEN=FLJ10716 /PROD=hypothetical protein FLJ10716 /DB_XREF=gi:8922616 /UG=Hs.24129 hypothetical protein FLJ10716 /FL=gb:NM_018191.1
213320_at	-2.22	Consensus includes gb:AL551971 /FEA=EST /DB_XREF=gi:12890422 /DB_XREF=est:AL551971 /CLONE=CS0DI060YG02 (3 prime) /UG=Hs.152337 protein arginine N-methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3
210621_s_at	-2.22	gb:M23612.1 /DEF=Human GTPase-activating protein (GAP) mRNA, complete cds. /FEA=mRNA /GEN=GAP /PROD=GTPase-activating protein /DB_XREF=gi:182973 /UG=Hs.758 RAS p21 protein activator (GTPase

		activating protein) 1 /FL=gb:NM_022650.1 gb:M23612.1
219976_at	-2.23	gb:NM_015888.1 /DEF=Homo sapiens hook1 protein (HOOK1), mRNA. /FEA=mRNA /GEN=HOOK1 /PROD=hook1 protein /DB_XREF=gi:7705414 /UG=Hs.250752 hook1 protein /FL=gb:AF044923.1 gb:NM_015888.1
218706_s_at	-2.23	Consensus includes gb:AW575493 /FEA=EST /DB_XREF=gi:7247032 /DB_XREF=est:UI-HF-BM0-adp-a-04-0-UI.s1 /CLONE=IMAGE:3062287 /UG=Hs.235445 hypothetical protein FLJ21313 /FL=gb:NM_023927.1
220936_s_at	-2.23	gb:NM_018267.1 /DEF=Homo sapiens hypothetical protein FLJ10903 (FLJ10903), mRNA. /FEA=mRNA /GEN=FLJ10903 /PROD=hypothetical protein FLJ10903 /DB_XREF=gi:8922757 /UG=Hs.36727 hypothetical protein FLJ10903 /FL=gb:NM_018267.1
213425_at	-2.23	Consensus includes gb:AI968085 /FEA=EST /DB_XREF=gi:5764903 /DB_XREF=est:wu12h08.x1 /CLONE=IMAGE:2516799 /UG=Hs.152213 wingless-type MMTV integration site family, member 5A
205768_s_at	-2.24	gb:NM_003645.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1), mRNA. /FEA=mRNA /GEN=FACVL1 /PROD=very long-chain fatty-acid-Coenzyme A ligase 1 /DB_XREF=gi:4503652 /UG=Hs.11729 fatty-acid-Coenzyme A ligase, very long-chain 1 /FL=gb:D88308.1 gb:AF096290.1 gb:NM_003645.1
207326_at	-2.24	gb:NM_001729.1 /DEF=Homo sapiens betacellulin (BTC), mRNA. /FEA=mRNA /GEN=BTC /PROD=betacellulin /DB_XREF=gi:4502460 /UG=Hs.73105 betacellulin /FL=gb:NM_001729.1
219957_at	-2.24	gb:NM_017987.1 /DEF=Homo sapiens hypothetical protein FLJ10063 (FLJ10063), mRNA. /FEA=mRNA /GEN=FLJ10063 /PROD=hypothetical protein FLJ10063 /DB_XREF=gi:8922215 /UG=Hs.154091 hypothetical protein FLJ10063 /FL=gb:NM_017987.1
218371_s_at	-2.25	gb:NM_018282.1 /DEF=Homo sapiens hypothetical protein FLJ10955 (FLJ10955), mRNA. /FEA=mRNA /GEN=FLJ10955 /PROD=hypothetical protein FLJ10955 /DB_XREF=gi:8922788 /UG=Hs.16364 hypothetical protein FLJ10955 /FL=gb:NM_018282.1
205194_at	-2.25	gb:NM_004577.1 /DEF=Homo sapiens phosphoserine phosphatase (PSPH), mRNA. /FEA=mRNA /GEN=PSPH /PROD=phosphoserine phosphatase /DB_XREF=gi:4758971 /UG=Hs.56407 phosphoserine phosphatase /FL=gb:NM_004577.1
212327_at	-2.25	Consensus includes gb:AK026815.1 /DEF=Homo sapiens cDNA: FLJ23162 fis, clone LNG09734. /FEA=mRNA /DB_XREF=gi:10439759 /UG=Hs.202949 KIAA1102 protein
213540_at	-2.26	Consensus includes gb:AL031228 /DEF=Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of ac... /FEA=mRNA_1 /DB_XREF=gi:3646023 /UG=Hs.288354 FabG (beta-ketoacyl-acyl-carrier-protein reductase, E coli) like
203169_at	-2.26	gb:NM_014785.1 /DEF=Homo sapiens KIAA0258 gene product (KIAA0258), mRNA. /FEA=mRNA /GEN=KIAA0258 /PROD=KIAA0258 gene product /DB_XREF=gi:7662029 /UG=Hs.47313 KIAA0258 gene product /FL=gb:BC001725.1 gb:D87447.1 gb:NM_014785.1
214440_at	-2.26	Consensus includes gb:NM_000662.1 /DEF=Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /FEA=CDS /GEN=NAT1 /PROD=N-acetyltransferase 1 /DB_XREF=gi:4505334 /UG=Hs.155956 N-acetyltransferase 1 (arylamine N-acetyltransferase) /FL=gb:NM_000662.1
218804_at	-2.26	gb:NM_018043.1 /DEF=Homo sapiens hypothetical protein FLJ10261 (FLJ10261), mRNA. /FEA=mRNA /GEN=FLJ10261 /PROD=hypothetical protein FLJ10261 /DB_XREF=gi:8922319 /UG=Hs.26176 hypothetical protein FLJ10261 /FL=gb:NM_018043.1
203232_s_at	-2.26	gb:NM_000332.1 /DEF=Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal

		dominant, ataxin 1) (SCA1), mRNA. /FEA=mRNA /GEN=SCA1 /PROD=ataxin 1 /DB_XREF=gi:4506792 /UG=Hs.74520 spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) /FL=gb:NM_000332.1
213110_s_at	-2.26	Consensus includes gb:AW052179 /FEA=EST /DB_XREF=gi:5914538 /DB_XREF=est:wx26h09.x1 /CLONE=IMAGE:2544833 /UG=Hs.169825 collagen, type IV, alpha 5 (Alport syndrome) /FL=gb:NM_000495.2
204838_s_at	-2.26	gb:NM_014381.1 /DEF=Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA. /FEA=mRNA /GEN=MLH3 /PROD=mutL (E. coli) homolog 3 /DB_XREF=gi:7657336 /UG=Hs.279843 mutL (E. coli) homolog 3 /FL=gb:AF195657.1 gb:NM_014381.1
216805_at	-2.26	Consensus includes gb:AK027254.1 /DEF=Homo sapiens cDNA: FLJ23601 fis, clone LNG15501. /FEA=mRNA /DB_XREF=gi:10440343 /UG=Hs.306918 Homo sapiens cDNA: FLJ23601 fis, clone LNG15501
208181_at	-2.27	gb:NM_003543.2 /DEF=Homo sapiens H4 histone family, member H (H4FH), mRNA. /FEA=mRNA /GEN=H4FH /PROD=H4 histone family, member H /DB_XREF=gi:5579466 /UG=Hs.93758 H4 histone family, member H /FL=gb:NM_003543.2
200704_at	-2.27	gb:AB034747.1 /DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. /FEA=mRNA /GEN=SIMPLE /PROD=small integral membrane protein of lysosomelateendosome /DB_XREF=gi:12862475 /UG=Hs.76507 LPS-induced TNF-alpha factor /FL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1 gb:NM_004862.1
209112_at	-2.27	gb:BC001971.1 /DEF=Homo sapiens, Similar to cyclin-dependent kinase inhibitor 1B (p27, Kip1), clone MGC:5304, mRNA, complete cds. /FEA=mRNA /PROD=Similar to cyclin-dependent kinase inhibitor 1B(p27, Kip1) /DB_XREF=gi:12805034 /UG=Hs.238990 cyclin-dependent kinase inhibitor 1B (p27, Kip1) /FL=gb:BC001971.1 gb:NM_004064.1 gb:U10906.1 gb:AF247551.1 gb:AY004255.1
203439_s_at	-2.27	gb:BC000658.1 /DEF=Homo sapiens, stanniocalcin 2, clone MGC:1881, mRNA, complete cds. /FEA=mRNA /PROD=stanniocalcin 2 /DB_XREF=gi:12653744 /UG=Hs.155223 stanniocalcin 2 /FL=gb:BC000658.1 gb:AF055460.1 gb:AB012664.1 gb:AF098462.1 gb:AF031036.1 gb:NM_003714.1
214007_s_at	-2.27	Consensus includes gb:AW665024 /FEA=EST /DB_XREF=gi:7457569 /DB_XREF=est:hi86c09.x1 /CLONE=IMAGE:2979184 /UG=Hs.82643 protein tyrosine kinase 9
206113_s_at	-2.27	gb:NM_004162.1 /DEF=Homo sapiens RAB5A, member RAS oncogene family (RAB5A), mRNA. /FEA=mRNA /GEN=RAB5A /PROD=RAB5A, member RAS oncogene family /DB_XREF=gi:4759003 /UG=Hs.73957 RAB5A, member RAS oncogene family /FL=gb:NM_004162.1 gb:M28215.1
209099_x_at	-2.28	gb:U73936.1 /DEF=Homo sapiens Jagged 1 (HJ1) mRNA, complete cds. /FEA=mRNA /GEN=HJ1 /PROD=Jagged 1 /DB_XREF=gi:1695273 /UG=Hs.91143 jagged 1 (Alagille syndrome) /FL=gb:U61276.1 gb:U73936.1 gb:AF003837.1 gb:AF028593.1 gb:NM_000214.1
215175_at	-2.29	Consensus includes gb:AB023212.1 /DEF=Homo sapiens mRNA for KIAA0995 protein, partial cds. /FEA=mRNA /GEN=KIAA0995 /PROD=KIAA0995 protein /DB_XREF=gi:4589633 /UG=Hs.225967 KIAA0995 protein
219608_s_at	-2.3	gb:NM_024862.1 /DEF=Homo sapiens hypothetical protein FLJ13962 (FLJ13962), mRNA. /FEA=mRNA /GEN=FLJ13962 /PROD=hypothetical protein FLJ13962 /DB_XREF=gi:13376291 /UG=Hs.330407 hypothetical protein FLJ13962 /FL=gb:NM_024862.1
214096_s_at	-2.31	Consensus includes gb:AW190316 /FEA=EST /DB_XREF=gi:6464796 /DB_XREF=est:xl13g08.x1 /CLONE=IMAGE:2676158 /UG=Hs.2186 eukaryotic translation elongation factor 1 gamma
202956_at	-2.31	gb:NM_006421.2 /DEF=Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA. /FEA=mRNA /GEN=BIG1 /PROD=brefeldin A-inhibited guaninenucleotide-exchange protein 1 /DB_XREF=gi:6715588 /UG=Hs.94631 brefeldin A-inhibited guanine nucleotide-exchange protein 1 /FL=gb:AF084520.1 gb:AF111162.1 gb:NM_006421.2

203227_s_at	-2.31	gb:NM_005981.1 /DEF=Homo sapiens sarcoma amplified sequence (SAS), mRNA. /FEA=mRNA /GEN=SAS /PROD=sarcoma amplified sequence /DB_XREF=gi:5174666 /UG=Hs.50984 sarcoma amplified sequence /FL=gb:U01160.1 gb:NM_005981.1
203895_at	-2.31	Consensus includes gb:AL535113 /FEA=EST /DB_XREF=gi:12798606 /DB_XREF=est:AL535113 /CLONE=CS0DF008YC23 (3 prime) /UG=Hs.283006 phospholipase C, beta 4 /FL=gb:NM_000933.1 gb:L41349.1
214831_at	-2.31	Consensus includes gb:AK024944.1 /DEF=Homo sapiens cDNA: FLJ21291 fis, clone COL01963. /FEA=mRNA /DB_XREF=gi:10437366 /UG=Hs.287657 Homo sapiens cDNA: FLJ21291 fis, clone COL01963
209210_s_at	-2.32	gb:Z24725.1 /DEF=H.sapiens mitogen inducible gene mig-2, complete CDS. /FEA=mRNA /PROD=mitogen inducible gene mig-2 /DB_XREF=gi:505032 /UG=Hs.75260 mitogen inducible 2 /FL=gb:Z24725.1
219581_at	-2.32	gb:NM_025265.1 /DEF=Homo sapiens hypothetical protein MGC2776 (MGC2776), mRNA. /FEA=mRNA /GEN=MGC2776 /PROD=hypothetical protein MGC2776 /DB_XREF=gi:13376881 /UG=Hs.15713 hypothetical protein MGC2776 /FL=gb:BC004178.1 gb:BC004211.1 gb:NM_025265.1
205219_s_at	-2.33	gb:NM_002044.1 /DEF=Homo sapiens galactokinase 2 (GALK2), mRNA. /FEA=mRNA /GEN=GALK2 /PROD=galactokinase 2 /DB_XREF=gi:4503896 /UG=Hs.129228 galactokinase 2 /FL=gb:BC005141.1 gb:M84443.1 gb:NM_002044.1
204672_s_at	-2.33	gb:NM_014942.1 /DEF=Homo sapiens KIAA0957 protein (KIAA0957), mRNA. /FEA=mRNA /GEN=KIAA0957 /PROD=KIAA0957 protein /DB_XREF=gi:7662405 /UG=Hs.30991 KIAA0957 protein /FL=gb:AB023174.1 gb:NM_014942.1
202342_s_at	-2.33	gb:NM_015271.1 /DEF=Homo sapiens tripartite motif protein TRIM2 (KIAA0517), mRNA. /FEA=mRNA /GEN=KIAA0517 /PROD=tripartite motif protein TRIM2 /DB_XREF=gi:13446226 /UG=Hs.12372 tripartite motif protein TRIM2 /FL=gb:AF220018.1 gb:NM_015271.1
216942_s_at	-2.33	Consensus includes gb:D28586.1 /DEF=Human mRNA for LFA-3(delta D2), partial cds. /FEA=mRNA /PROD=LFA-3(delta D2) /DB_XREF=gi:466540 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3)
215723_s_at	-2.34	Consensus includes gb:AJ276230.1 /DEF=Homo sapiens mRNA for partial phospholipase D1, splice variant PLD1ab2. /FEA=mRNA /GEN=PLD1 /PROD=phospholipase D1 /DB_XREF=gi:7161182 /UG=Hs.82587 phospholipase D1, phophatidylcholine-specific
213501_at	-2.34	Consensus includes gb:T62985 /FEA=EST /DB_XREF=gi:666642 /DB_XREF=est:yc15d05.s1 /CLONE=IMAGE:80745 /UG=Hs.167835 acyl-Coenzyme A oxidase 1, palmitoyl
207416_s_at	-2.34	gb:NM_004555.1 /DEF=Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), mRNA. /FEA=mRNA /GEN=NFATC3 /PROD=nuclear factor of activated T-cells,cytoplasmic, calcineurin-dependent 3 /DB_XREF=gi:4758803 /UG=Hs.172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:U85428.1 gb:NM_004555.1 gb:L41067.1
203570_at	-2.34	gb:NM_005576.1 /DEF=Homo sapiens lysyl oxidase-like 1 (LOXL1), mRNA. /FEA=mRNA /GEN=LOXL1 /PROD=lysyl oxidase-like 1 /DB_XREF=gi:5031882 /UG=Hs.65436 lysyl oxidase-like 1 /FL=gb:L21186.1 gb:NM_005576.1
218877_s_at	-2.35	gb:NM_021820.1 /DEF=Homo sapiens MDS024 protein (MDS024), mRNA. /FEA=mRNA /GEN=MDS024 /PROD=MDS024 protein /DB_XREF=gi:11141892 /UG=Hs.286122 MDS024 protein /FL=gb:AF182423.1 gb:NM_021820.1
220122_at	-2.35	gb:NM_024717.1 /DEF=Homo sapiens hypothetical protein FLJ22344 (FLJ22344), mRNA. /FEA=mRNA /GEN=FLJ22344 /PROD=hypothetical protein FLJ22344 /DB_XREF=gi:13376020 /UG=Hs.107716 hypothetical protein FLJ22344 /FL=gb:NM_024717.1
220089_at	-2.35	gb:NM_024884.1 /DEF=Homo sapiens hypothetical protein FLJ12618 (FLJ12618), mRNA. /FEA=mRNA /GEN=FLJ12618 /PROD=hypothetical protein FLJ12618 /DB_XREF=gi:13376330 /UG=Hs.222021 hypothetical

		protein FLJ12618 /FL=gb:NM_024884.1
218701_at	-2.36	gb:NM_016027.1 /DEF=Homo sapiens CGI-83 protein (LOC51110), mRNA. /FEA=mRNA /GEN=LOC51110 /PROD=CGI-83 protein /DB_XREF=gi:7705792 /UG=Hs.118554 CGI-83 protein /FL=gb:BC000878.1 gb:AF151841.1 gb:NM_016027.1
218545_at	-2.37	gb:NM_018318.1 /DEF=Homo sapiens hypothetical protein FLJ11088 (FLJ11088), mRNA. /FEA=mRNA /GEN=FLJ11088 /PROD=hypothetical protein FLJ11088 /DB_XREF=gi:8922858 /UG=Hs.49282 hypothetical protein FLJ11088 /FL=gb:NM_018318.1
207713_s_at	-2.37	gb:NM_006462.1 /DEF=Homo sapiens HBV associated factor (XAP4), mRNA. /FEA=mRNA /GEN=XAP4 /PROD=HBV associated factor /DB_XREF=gi:5454167 /UG=Hs.247280 HBV associated factor /FL=gb:NM_006462.1
202149_at	-2.37	Consensus includes gb:AL136139 /DEF=Human DNA sequence from clone RP4-761I2 on chromosome 6 Contains 3 part of the gene for enhancer of filamentation (HEF1), ESTs, STSs and CpG islands /FEA=mRNA /DB_XREF=gi:8217463 /UG=Hs.80261 enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) /FL=gb:L43821.1 gb:U64317.1 gb:NM_006403.1
206101_at	-2.37	gb:NM_001393.1 /DEF=Homo sapiens extracellular matrix protein 2, female organ and adipocyte specific (ECM2), mRNA. /FEA=mRNA /GEN=ECM2 /PROD=extracellular matrix protein 2 /DB_XREF=gi:4557542 /UG=Hs.35094 extracellular matrix protein 2, female organ and adipocyte specific /FL=gb:AB011792.1 gb:NM_001393.1
205087_at	-2.38	gb:NM_015485.1 /DEF=Homo sapiens DKFZP566K023 protein (DKFZP566K023), mRNA. /FEA=mRNA /GEN=DKFZP566K023 /PROD=DKFZP566K023 protein /DB_XREF=gi:7661655 /UG=Hs.19999 DKFZP566K023 protein /FL=gb:NM_015485.1
204040_at	-2.39	gb:NM_014746.1 /DEF=Homo sapiens KIAA0161 gene product (KIAA0161), mRNA. /FEA=mRNA /GEN=KIAA0161 /PROD=KIAA0161 gene product /DB_XREF=gi:7661955 /UG=Hs.78894 KIAA0161 gene product /FL=gb:D79983.1 gb:NM_014746.1
210510_s_at	-2.39	gb:AF145712.1 /DEF=Homo sapiens soluble neuropilin-1 mRNA, complete cds. /FEA=mRNA /PROD=soluble neuropilin-1 /DB_XREF=gi:7271464 /UG=Hs.69285 neuropilin 1 /FL=gb:AF145712.1
220072_at	-2.39	gb:NM_024790.1 /DEF=Homo sapiens hypothetical protein FLJ22490 (FLJ22490), mRNA. /FEA=mRNA /GEN=FLJ22490 /PROD=hypothetical protein FLJ22490 /DB_XREF=gi:13376157 /UG=Hs.153746 hypothetical protein FLJ22490 /FL=gb:NM_024790.1
218197_s_at	-2.39	gb:NM_018002.1 /DEF=Homo sapiens oxidation resistance 1 (OXR1), mRNA. /FEA=mRNA /GEN=OXR1 /PROD=oxidation resistance 1 /DB_XREF=gi:8922240 /UG=Hs.169111 oxidation resistance 1 /FL=gb:NM_018002.1
219109_at	-2.4	gb:NM_024532.1 /DEF=Homo sapiens hypothetical protein FLJ22724 (FLJ22724), mRNA. /FEA=mRNA /GEN=FLJ22724 /PROD=hypothetical protein FLJ22724 /DB_XREF=gi:13375683 /UG=Hs.6783 hypothetical protein FLJ22724 /FL=gb:NM_024532.1
216411_s_at	-2.4	Consensus includes gb:AK023699.1 /DEF=Homo sapiens cDNA FLJ13637 fis, clone PLACE1011165. /FEA=mRNA /DB_XREF=gi:10435704 /UG=Hs.287584 Homo sapiens cDNA FLJ13637 fis, clone PLACE1011165
213419_at	-2.41	Consensus includes gb:U62325.1 /DEF=Human FE65-like protein (hFE65L) mRNA, partial cds. /FEA=mRNA /GEN=hFE65L /PROD=FE65-like protein /DB_XREF=gi:1657751 /UG=Hs.324125 amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
212338_at	-2.41	Consensus includes gb:AA621962 /FEA=EST /DB_XREF=gi:2525838 /DB_XREF=est:nq24b02.s1 /CLONE=IMAGE:1144779 /UG=Hs.39871 KIAA0727 protein
212870_at	-2.41	Consensus includes gb:AI628605 /FEA=EST /DB_XREF=gi:4665405 /DB_XREF=est:ty77a08.x1 /CLONE=IMAGE:2285078 /UG=Hs.326392 son of sevenless (Drosophila) homolog 1 /FL=gb:L13858.1

		gb:NM_005633.1
213839_at	-2.41	Consensus includes gb:AW028110 /FEA=EST /DB_XREF=gi:5886866 /DB_XREF=est:wv26a10.x1 /CLONE=IMAGE:2530650 /UG=Hs.301478 KIAA0500 protein
219280_at	-2.41	gb:NM_018963.1 /DEF=Homo sapiens WD repeat domain 9 (WDR9), mRNA. /FEA=mRNA /GEN=WDR9 /PROD=WD repeat domain 9 /DB_XREF=gi:11321643 /UG=Hs.225674 WD repeat domain 9 /FL=gb:NM_018963.1
221730_at	-2.41	Consensus includes gb:NM_000393.1 /DEF=Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA. /FEA=CDS /GEN=COL5A2 /PROD=collagen, type V, alpha 2 /DB_XREF=gi:4502958 /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393.1
209189_at	-2.43	gb:BC004490.1 /DEF=Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074, mRNA, complete cds. /FEA=mRNA /PROD=v-fos FBJ murine osteosarcoma viral oncogenehomolog /DB_XREF=gi:13325363 /UG=Hs.25647 v-fos FBJ murine osteosarcoma viral oncogene homolog /FL=gb:BC004490.1 gb:NM_005252.2
203513_at	-2.43	gb:NM_025137.1 /DEF=Homo sapiens hypothetical protein FLJ21439 (FLJ21439), mRNA. /FEA=mRNA /GEN=FLJ21439 /PROD=hypothetical protein FLJ21439 /DB_XREF=gi:13376718 /UG=Hs.288872 hypothetical protein FLJ21439 /FL=gb:NM_025137.1
221824_s_at	-2.43	Consensus includes gb:AA770170 /FEA=EST /DB_XREF=gi:2821408 /DB_XREF=est:ah84d09.s1 /CLONE=1322321 /UG=Hs.288156 Homo sapiens cDNA: FLJ21819 fis, clone HEP01185
203780_at	-2.44	gb:AF275945.1 /DEF=Homo sapiens epithelial V-like antigen 1 (EVA1) mRNA, complete cds. /FEA=mRNA /GEN=EVA1 /PROD=epithelial V-like antigen 1 /DB_XREF=gi:9392652 /UG=Hs.116651 epithelial V-like antigen 1 /FL=gb:AF304447.1 gb:AF030455.1 gb:NM_005797.1 gb:AF275945.1
220945_x_at	-2.44	gb:NM_018050.1 /DEF=Homo sapiens hypothetical protein FLJ10298 (FLJ10298), mRNA. /FEA=mRNA /GEN=FLJ10298 /PROD=hypothetical protein FLJ10298 /DB_XREF=gi:8922334 /UG=Hs.5999 hypothetical protein FLJ10298 /FL=gb:NM_018050.1
207219_at	-2.44	gb:NM_023070.1 /DEF=Homo sapiens hypothetical protein (LOC65243), mRNA. /FEA=mRNA /GEN=LOC65243 /PROD=hypothetical protein /DB_XREF=gi:12751478 /UG=Hs.133034 hypothetical protein /FL=gb:NM_023070.1
217627_at	-2.45	Consensus includes gb:BE515346 /FEA=EST /DB_XREF=gi:9722561 /DB_XREF=est:601235986F1 /CLONE=IMAGE:3608205 /UG=Hs.278871 ESTs, Weakly similar to S47072 finger protein HZF10, Krueppel-related H.sapiens
61732_r_at	-2.46	Cluster Incl. AI610355:tp18g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2188190 /clone_end=3 /gb=AI610355 /gi=4619522 /ug=Hs.39328 /len=463
209457_at	-2.46	gb:U16996.1 /DEF=Human protein tyrosine phosphatase mRNA, complete cds. /FEA=mRNA /PROD=protein tyrosine phosphatase /DB_XREF=gi:642012 /UG=Hs.2128 dual specificity phosphatase 5 /FL=gb:NM_004419.2 gb:U16996.1 gb:U15932.2
213308_at	-2.46	Consensus includes gb:BF435773 /FEA=EST /DB_XREF=gi:11448088 /DB_XREF=est:nab41f03.x1 /CLONE=IMAGE:3268373 /UG=Hs.12696 cortactin SH3 domain-binding protein
220176_at	-2.46	gb:NM_025152.1 /DEF=Homo sapiens hypothetical protein FLJ12660 (FLJ12660), mRNA. /FEA=mRNA /GEN=FLJ12660 /PROD=hypothetical protein FLJ12660 /DB_XREF=gi:13376746 /UG=Hs.288981 hypothetical protein FLJ12660 /FL=gb:NM_025152.1
205594_at	-2.46	gb:NM_014897.1 /DEF=Homo sapiens KIAA0924 protein (KIAA0924), mRNA. /FEA=mRNA /GEN=KIAA0924 /PROD=KIAA0924 protein /DB_XREF=gi:7662383 /UG=Hs.190386 KIAA0924 protein /FL=gb:AB023141.1 gb:NM_014897.1
215022_x_at	-2.47	Consensus includes gb:BG429214 /FEA=EST /DB_XREF=gi:13335720 /DB_XREF=est:602498083F1 /CLONE=IMAGE:4611836 /UG=Hs.258144 zinc finger protein 33b (KOX 31)

215610_at	-2.48	Consensus includes gb:AK022038.1 /DEF=Homo sapiens cDNA FLJ11976 fis, clone HEMBB1001253. /FEA=mRNA /DB_XREF=gi:10433356 /UG=Hs.296679 Homo sapiens cDNA FLJ11976 fis, clone HEMBB1001253
218043_s_at	-2.48	gb:NM_022461.1 /DEF=Homo sapiens hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 (FLJ21939), mRNA. /FEA=mRNA /GEN=FLJ21939 /PROD=hypothetical protein FLJ21939 similar to5-azacytidine induced gene 2 /DB_XREF=gi:11968002 /UG=Hs.164478 hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 /FL=gb:NM_022461.1
209551_at	-2.48	gb:BC004875.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2310034L04 gene /DB_XREF=gi:13436109 /UG=Hs.66309 Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds /FL=gb:BC004875.1
213212_x_at	-2.48	Consensus includes gb:AI632181 /FEA=EST /DB_XREF=gi:4683511 /DB_XREF=est:ts85h05.x1 /CLONE=IMAGE:2238105 /UG=Hs.182982 golgin-67
206506_s_at	-2.48	gb:NM_003599.1 /DEF=Homo sapiens suppressor of Ty (S.cerevisiae) 3 homolog (SUPT3H), mRNA. /FEA=mRNA /GEN=SUPT3H /PROD=suppressor of Ty (S.cerevisiae) 3 homolog /DB_XREF=gi:4507308 /UG=Hs.96757 suppressor of Ty (S.cerevisiae) 3 homolog /FL=gb:AF073930.1 gb:AF069734.1 gb:NM_003599.1
204671_s_at	-2.48	Consensus includes gb:BE677131 /FEA=EST /DB_XREF=gi:10037672 /DB_XREF=est:7d80g06.x1 /CLONE=IMAGE:3279322 /UG=Hs.30991 KIAA0957 protein /FL=gb:AB023174.1 gb:NM_014942.1
205042_at	-2.48	gb:NM_005476.2 /DEF=Homo sapiens UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase (GNE), mRNA. /FEA=mRNA /GEN=GNE /PROD=UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase /DB_XREF=gi:6382074 /UG=Hs.5920 UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase /FL=gb:AF051852.1 gb:AF155663.1 gb:NM_005476.2
217915_s_at	-2.49	gb:NM_016304.1 /DEF=Homo sapiens 60S ribosomal protein L30 isolog (LOC51187), mRNA. /FEA=mRNA /GEN=LOC51187 /PROD=60S ribosomal protein L30 isolog /DB_XREF=gi:10047101 /UG=Hs.284162 60S ribosomal protein L30 isolog /FL=gb:NM_016304.1 gb:AF060926.1 gb:AF212226.1 gb:BC005344.1 gb:AF201949.1 gb:AF165521.1
204554_at	-2.49	Consensus includes gb:AL109928 /DEF=Human DNA sequence from clone RP4-551D2 on chromosome 20q13.2-13.33. Contains the gene for a novel Cadherin domain protein, a novel gene, the PPP1R6 gene for protein phosphatase 1 regulatory subunit 6, the 5 end of the SYCP2 gene for synaptonemal... /FEA=mRNA_6 /DB_XREF=gi:7981303 /UG=Hs.42215 protein phosphatase 1, regulatory subunit 6 /FL=gb:NM_006242.2
204205_at	-2.49	gb:NM_021822.1 /DEF=Homo sapiens phorbolin-like protein MDS019 (MDS019), mRNA. /FEA=mRNA /GEN=MDS019 /PROD=phorbolin-like protein MDS019 /DB_XREF=gi:13399303 /UG=Hs.250619 phorbolin-like protein MDS019 /FL=gb:AF182420.1 gb:NM_021822.1
215163_at	-2.5	Consensus includes gb:AK022211.1 /DEF=Homo sapiens cDNA FLJ12149 fis, clone MAMMA1000421. /FEA=mRNA /DB_XREF=gi:10433557 /UG=Hs.203349 Homo sapiens cDNA FLJ12149 fis, clone MAMMA1000421
206667_s_at	-2.5	gb:AF005037.1 /DEF=Homo sapiens secretory carrier membrane protein (SCAMP1) mRNA, complete cds. /FEA=mRNA /GEN=SCAMP1 /PROD=secretory carrier membrane protein /DB_XREF=gi:2232238 /UG=Hs.31218 secretory carrier membrane protein 1 /FL=gb:AF005037.1 gb:AF038966.1 gb:NM_004866.1
203186_s_at	-2.5	gb:NM_002961.2 /DEF=Homo sapiens S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), transcript variant 1, mRNA. /FEA=mRNA /GEN=S100A4 /PROD=S100 calcium-binding protein A4 /DB_XREF=gi:9845514 /UG=Hs.81256 S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) /FL=gb:NM_002961.2 gb:NM_019554.1
216470_x_at	-2.5	Consensus includes gb:AF009664 /DEF=Homo sapiens T cell receptor beta locus, 3 trypsinogen repeats /FEA=CDS_1 /DB_XREF=gi:2275594 /UG=Hs.303157 T cell receptor beta locus

205280_at	-2.51	gb:NM_000824.1 /DEF=Homo sapiens glycine receptor, beta (GLRB), mRNA. /FEA=mRNA /GEN=GLRB /PROD=glycine receptor, beta /DB_XREF=gi:4504022 /UG=Hs.32973 glycine receptor, beta /FL=gb:AF094754.1 gb:NM_000824.1 gb:U33267.1
202538_s_at	-2.51	gb:NM_014043.1 /DEF=Homo sapiens DKFZP564O123 protein (DKFZP564O123), mRNA. /FEA=mRNA /GEN=DKFZP564O123 /PROD=DKFZP564O123 protein /DB_XREF=gi:7661633 /UG=Hs.11449 DKFZP564O123 protein /FL=gb:AF151842.1 gb:AL080122.1 gb:NM_014043.1
207836_s_at	-2.53	gb:NM_006867.1 /DEF=Homo sapiens RNA-binding protein gene with multiple splicing (RBPMS), mRNA. /FEA=mRNA /GEN=RBPMS /PROD=RNA-binding protein gene with multiple splicing /DB_XREF=gi:5803140 /UG=Hs.80248 RNA-binding protein gene with multiple splicing /FL=gb:D84110.1 gb:NM_006867.1
203917_at	-2.53	gb:NM_001338.1 /DEF=Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA. /FEA=mRNA /GEN=CXADR /PROD=coxsackie virus and adenovirus receptor /DB_XREF=gi:4503172 /UG=Hs.79187 coxsackie virus and adenovirus receptor /FL=gb:BC003684.1 gb:U90716.1 gb:NM_001338.1
221986_s_at	-2.53	Consensus includes gb:AW006750 /FEA=EST /DB_XREF=gi:5855528 /DB_XREF=est:wr28h09.x1 /CLONE=IMAGE:2489057 /UG=Hs.246875 hypothetical protein FLJ20059
218176_at	-2.53	gb:NM_022149.1 /DEF=Homo sapiens MAGEF1 protein (MAGEF1), mRNA. /FEA=mRNA /GEN=MAGEF1 /PROD=MAGEF1 protein /DB_XREF=gi:11545891 /UG=Hs.306123 MAGEF1 protein /FL=gb:AF295378.1 gb:NM_022149.1
218919_at	-2.54	gb:NM_024699.1 /DEF=Homo sapiens hypothetical protein FLJ14007 (FLJ14007), mRNA. /FEA=mRNA /GEN=FLJ14007 /PROD=hypothetical protein FLJ14007 /DB_XREF=gi:13375984 /UG=Hs.99519 hypothetical protein FLJ14007 /FL=gb:NM_024699.1
211555_s_at	-2.54	gb:AF020340.1 /DEF=Homo sapiens soluble guanylate cyclase beta-1 subunit (GC-S-beta-1) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=GC-S-beta-1 /PROD=soluble guanylate cyclase beta-1 subunit /DB_XREF=gi:2746082 /UG=Hs.77890 guanylate cyclase 1, soluble, beta 3 /FL=gb:AF020340.1
222148_s_at	-2.54	Consensus includes gb:BF688108 /FEA=EST /DB_XREF=gi:11973516 /DB_XREF=est:602067332F1 /CLONE=IMAGE:4066422 /UG=Hs.14202 hypothetical protein FLJ11040
213376_at	-2.54	Consensus includes gb:AI656706 /FEA=EST /DB_XREF=gi:4740685 /DB_XREF=est:tt53e01.x1 /CLONE=IMAGE:2244504 /UG=Hs.24083 KIAA0997 protein
201811_x_at	-2.54	gb:NM_004844.1 /DEF=Homo sapiens SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA. /FEA=mRNA /GEN=SH3BP5 /PROD=SH3-domain binding protein 5 (BTK-associated) /DB_XREF=gi:4759057 /UG=Hs.109150 SH3-domain binding protein 5 (BTK-associated) /FL=gb:AB005047.1 gb:NM_004844.1
218035_s_at	-2.55	gb:NM_019027.1 /DEF=Homo sapiens hypothetical protein (FLJ20273), mRNA. /FEA=mRNA /GEN=FLJ20273 /PROD=hypothetical protein /DB_XREF=gi:9506670 /UG=Hs.95549 hypothetical protein /FL=gb:NM_019027.1
210480_s_at	-2.55	gb:U90236.2 /DEF=Homo sapiens myosin VI (MYO6) mRNA, complete cds. /FEA=mRNA /GEN=MYO6 /PROD=myosin VI /DB_XREF=gi:9280815 /UG=Hs.22564 myosin VI /FL=gb:U90236.2
203408_s_at	-2.55	gb:NM_002971.1 /DEF=Homo sapiens special AT-rich sequence binding protein 1 (binds to nuclear matrixscaffold-associating DNAs) (SATB1), mRNA. /FEA=mRNA /GEN=SATB1 /PROD=special AT-rich sequence binding protein 1(binds to nuclear matrixscaffold-associating DNAs) /DB_XREF=gi:4506790 /UG=Hs.74592 special AT-rich sequence binding protein 1 (binds to nuclear matrixscaffold-associating DNAs) /FL=gb:M97287.1 gb:NM_002971.1
215707_s_at	-2.55	Consensus includes gb:AV725328 /FEA=EST /DB_XREF=gi:10830606 /DB_XREF=est:AV725328 /CLONE=HTCAVD03 /UG=Hs.74621 prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
204068_at	-2.55	gb:NM_006281.1 /DEF=Homo sapiens serinethreonine kinase 3 (Ste20, yeast homolog) (STK3), mRNA. /FEA=mRNA /GEN=STK3 /PROD=serinethreonine kinase 3 (Ste20, yeasthomolog) /DB_XREF=gi:5454093

		/UG=Hs.166684 serinethreonine kinase 3 (Ste20, yeast homolog) /FL=gb:U26424.1 gb:U60206.1 gb:NM_006281.1
203988_s_at	-2.55	gb:NM_004480.1 /DEF=Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA. /FEA=mRNA /GEN=FUT8 /PROD=fucosyltransferase 8 (alpha (1,6)fucosyltransferase) /DB_XREF=gi:4758407 /UG=Hs.118722 fucosyltransferase 8 (alpha (1,6) fucosyltransferase) /FL=gb:D89289.1 gb:NM_004480.1
222266_at	-2.55	Consensus includes gb:BF796940 /FEA=EST /DB_XREF=gi:12101994 /DB_XREF=est:602258153F1 /CLONE=IMAGE:4341588 /UG=Hs.294100 ESTs
203608_at	-2.56	Consensus includes gb:AL031230 /DEF=Human DNA sequence from clone 73M23 on chromosome 6p22.2-22.3. Contains the 5 part of the possibly alternatively spliced gene for Phosphatidylinositol-glycan-specific Phospholipase D 1 precursor (EC 3.1.4.50, PIGPLD1, Glycoprotein Phospholipase D... /FEA=mRNA_5 /DB_XREF=gi:3947845 /UG=Hs.5299 aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) /FL=gb:NM_001080.1
211937_at	-2.56	Consensus includes gb:NM_001417.1 /DEF=Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA. /FEA=CDS /GEN=EIF4B /PROD=eukaryotic translation initiation factor 4B /DB_XREF=gi:4503532 /UG=Hs.93379 eukaryotic translation initiation factor 4B /FL=gb:NM_001417.1
212633_at	-2.56	Consensus includes gb:AL132776 /DEF=Human DNA sequence from clone RP3-393D12 on chromosome 6q16.1-16.3. Contains the 3 end of the gene KIAA0776, the gene for a novel LIM domain protein, ESTs, STSs and GSSs /FEA=mRNA_2 /DB_XREF=gi:6706246 /UG=Hs.5460 KIAA0776 protein
220169_at	-2.56	gb:NM_024943.1 /DEF=Homo sapiens hypothetical protein FLJ23235 (FLJ23235), mRNA. /FEA=mRNA /GEN=FLJ23235 /PROD=hypothetical protein FLJ23235 /DB_XREF=gi:13376422 /UG=Hs.283578 hypothetical protein FLJ23235 /FL=gb:NM_024943.1
221085_at	-2.56	gb:NM_005118.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 15 (TNFSF15), mRNA. /FEA=mRNA /GEN=TNFSF15 /PROD=tumor necrosis factor (ligand) superfamily,member 15 /DB_XREF=gi:4827031 /UG=Hs.241382 tumor necrosis factor (ligand) superfamily, member 15 /FL=gb:NM_005118.1
203989_x_at	-2.57	gb:NM_001992.2 /DEF=Homo sapiens coagulation factor II (thrombin) receptor (F2R), mRNA. /FEA=mRNA /GEN=F2R /PROD=coagulation factor II receptor precursor /DB_XREF=gi:6031164 /UG=Hs.128087 coagulation factor II (thrombin) receptor /FL=gb:BC002464.1 gb:M62424.1 gb:NM_001992.2
211277_x_at	-2.57	gb:BC004369.1 /DEF=Homo sapiens, Similar to amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease), clone MGC:10403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to amyloid beta (A4) precursor protein(protease nexin-II, Alzheimer disease) /DB_XREF=gi:13325111 /UG=Hs.177486 amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) /FL=gb:BC004369.1
218645_at	-2.58	gb:NM_021994.1 /DEF=Homo sapiens zinc finger protein 277 (ZNF277), mRNA. /FEA=mRNA /GEN=ZNF277 /PROD=zinc finger protein 277 /DB_XREF=gi:11496268 /UG=Hs.42636 zinc finger protein 277 /FL=gb:NM_021994.1 gb:AF209198.1
215785_s_at	-2.58	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mRNA /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein
214182_at	-2.58	Consensus includes gb:AA243143 /FEA=EST /DB_XREF=gi:1874138 /DB_XREF=est:zs13h04.s1 /CLONE=IMAGE:685111 /UG=Hs.89474 ADP-ribosylation factor 6
209212_s_at	-2.58	gb:AB030824.1 /DEF=Homo sapiens mRNA for transcription factor BTEB2, complete cds. /FEA=mRNA /GEN=bteb2 /PROD=transcription factor BTEB2 /DB_XREF=gi:8272417 /UG=Hs.84728 Kruppel-like factor 5 (intestinal) /FL=gb:D14520.1 gb:NM_001730.1 gb:AF132818.1 gb:AB030824.1 gb:AF287272.1
215294_s_at	-2.58	Consensus includes gb:AK026426.1 /DEF=Homo sapiens cDNA: FLJ22773 fis, clone KAIA1473, highly similar to

		HUMSNF2L Human global transcription activator homologous sequence mRNA. /FEA=mRNA /DB_XREF=gi:10439287 /UG=Hs.152292 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
218311_at	-2.58	gb:NM_003618.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /FEA=mRNA /GEN=MAP4K3 /PROD=mitogen-activated protein kinase kinase kinasekinase 3 /DB_XREF=gi:4506376 /UG=Hs.227400 mitogen-activated protein kinase kinase kinase kinase 3 /FL=gb:AF000145.1 gb:NM_003618.1
209625_at	-2.59	gb:BC004100.1 /DEF=Homo sapiens, phosphatidylinositol glycan, class H, clone MGC:10360, mRNA, complete cds. /FEA=mRNA /PROD=phosphatidylinositol glycan, class H /DB_XREF=gi:13278629 /UG=Hs.177 phosphatidylinositol glycan, class H /FL=gb:BC004100.1 gb:L19783.1 gb:NM_004569.1
212299_at	-2.59	Consensus includes gb:AL117502.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935). /FEA=mRNA /DB_XREF=gi:5912009 /UG=Hs.7200 Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935)
212593_s_at	-2.61	Consensus includes gb:N92498 /FEA=EST /DB_XREF=gi:1264807 /DB_XREF=est:zb28a04.s1 /CLONE=IMAGE:304878 /UG=Hs.326248 Homo sapiens cDNA: FLJ22071 fis, clone HEP11691
215395_x_at	-2.61	Consensus includes gb:U66061 /DEF=Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRB... /FEA=CDS_1 /DB_XREF=gi:1552511 /UG=Hs.302180 Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, TC
221268_s_at	-2.61	gb:NM_030791.1 /DEF=Homo sapiens sphingosine-1-phosphatase (LOC81537), mRNA. /FEA=mRNA /GEN=LOC81537 /PROD=sphingosine-1-phosphatase /DB_XREF=gi:13540568 /FL=gb:NM_030791.1
211760_s_at	-2.62	gb:BC005974.1 /DEF=Homo sapiens, vesicle-associated membrane protein 4, clone MGC:14658, mRNA, complete cds. /FEA=mRNA /PROD=vesicle-associated membrane protein 4 /DB_XREF=gi:13543647 /FL=gb:BC005974.1
203265_s_at	-2.62	Consensus includes gb:AA810268 /FEA=EST /DB_XREF=gi:2879627 /DB_XREF=est:od14f07.s1 /CLONE=IMAGE:1367941 /UG=Hs.75217 mitogen-activated protein kinase kinase 4 /FL=gb:NM_003010.1 gb:L36870.1 gb:U17743.1
218665_at	-2.62	gb:NM_012193.1 /DEF=Homo sapiens frizzled (Drosophila) homolog 4 (FZD4), mRNA. /FEA=mRNA /GEN=FZD4 /PROD=frizzled (Drosophila) homolog 4 /DB_XREF=gi:6912383 /UG=Hs.19545 frizzled (Drosophila) homolog 4 /FL=gb:AB032417.1 gb:NM_012193.1
206417_at	-2.65	gb:NM_000087.1 /DEF=Homo sapiens cyclic nucleotide gated channel alpha 1 (CNGA1), mRNA. /FEA=mRNA /GEN=CNGA1 /PROD=cyclic nucleotide gated channel alpha 1 /DB_XREF=gi:4502914 /UG=Hs.1323 cyclic nucleotide gated channel alpha 1 /FL=gb:M84741.1 gb:NM_000087.1
213704_at	-2.66	Consensus includes gb:AA129753 /FEA=EST /DB_XREF=gi:1690163 /DB_XREF=est:zl16a12.s1 /CLONE=IMAGE:502078 /UG=Hs.78948 Rab geranylgeranyltransferase, beta subunit
204351_at	-2.67	gb:NM_005980.1 /DEF=Homo sapiens S100 calcium-binding protein P (S100P), mRNA. /FEA=mRNA /GEN=S100P /PROD=S100 calcium-binding protein P /DB_XREF=gi:5174662 /UG=Hs.2962 S100 calcium-binding protein P /FL=gb:NM_005980.1
205402_x_at	-2.68	gb:NM_002770.1 /DEF=Homo sapiens protease, serine, 2 (trypsin 2) (PRSS2), mRNA. /FEA=mRNA /GEN=PRSS2 /PROD=protease, serine, 2 (trypsin 2) /DB_XREF=gi:4506146 /UG=Hs.241561 protease, serine, 2 (trypsin 2) /FL=gb:NM_002770.1 gb:M27602.1

65517_at	-2.68	Cluster Incl. AA910946:ok85g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1520794 /clone_end=3 /gb=AA910946 /gi=3050236 /ug=Hs.18894 /len=982
213672_at	-2.7	Consensus includes gb:AA621558 /FEA=EST /DB_XREF=gi:2525497 /DB_XREF=est:af53a09.s1 /CLONE=IMAGE:1035352 /UG=Hs.279946 methionine-tRNA synthetase
210802_s_at	-2.7	gb:BC002841.1 /DEF=Homo sapiens, Similar to putative dimethyladenosine transferase, clone MGC:3382, mRNA, complete cds. /FEA=mRNA /PROD=Similar to putative dimethyladenosinetransferase /DB_XREF=gi:12803982 /UG=Hs.125819 putative dimethyladenosine transferase /FL=gb:BC002841.1
219270_at	-2.71	gb:NM_024111.1 /DEF=Homo sapiens hypothetical protein MGC4504 (MGC4504), mRNA. /FEA=mRNA /GEN=MGC4504 /PROD=hypothetical protein MGC4504 /DB_XREF=gi:13129125 /UG=Hs.155569 hypothetical protein MGC4504 /FL=gb:BC001847.1 gb:NM_024111.1
206354_at	-2.71	gb:NM_019844.1 /DEF=Homo sapiens solute carrier family 21 (organic anion transporter), member 8 (SLC21A8), mRNA. /FEA=mRNA /GEN=SLC21A8 /PROD=solute carrier family 21 (organic aniontransporter), member 8 /DB_XREF=gi:9790232 /UG=Hs.274981 solute carrier family 21 (organic anion transporter), member 8 /FL=gb:AF187815.1 gb:NM_019844.1
213421_x_at	-2.71	Consensus includes gb:AW007273 /FEA=EST /DB_XREF=gi:5856051 /DB_XREF=est:wt54d10.x1 /CLONE=IMAGE:2511283 /UG=Hs.58247 protease, serine, 4 (trypsin 4, brain)
219429_at	-2.72	gb:NM_024306.1 /DEF=Homo sapiens fatty acid hydroxylase (FAAH), mRNA. /FEA=mRNA /GEN=FAAH /PROD=fatty acid hydroxylase /DB_XREF=gi:13236537 /UG=Hs.249163 fatty acid hydroxylase /FL=gb:BC002679.1 gb:NM_024306.1 gb:BC004263.1
217564_s_at	-2.72	Consensus includes gb:W80357 /FEA=EST /DB_XREF=gi:1391394 /DB_XREF=est:zh49a06.s1 /CLONE=IMAGE:415378 /UG=Hs.326685 Homo sapiens carbamoyl-phosphate synthetase 1, mitochondrial (CPS1), mRNA
220728_at	-2.72	gb:NM_025120.1 /DEF=Homo sapiens hypothetical protein FLJ13480 (FLJ13480), mRNA. /FEA=mRNA /GEN=FLJ13480 /PROD=hypothetical protein FLJ13480 /DB_XREF=gi:13376698 /UG=Hs.288734 hypothetical protein FLJ13480 /FL=gb:NM_025120.1
218779_x_at	-2.73	gb:NM_017729.1 /DEF=Homo sapiens hypothetical protein FLJ20258 (FLJ20258), mRNA. /FEA=mRNA /GEN=FLJ20258 /PROD=hypothetical protein FLJ20258 /DB_XREF=gi:8923231 /UG=Hs.28907 hypothetical protein FLJ20258 /FL=gb:NM_017729.1
206385_s_at	-2.73	gb:NM_020987.1 /DEF=Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA. /FEA=mRNA /GEN=ANK3 /PROD=ankyrin 3, isoform 1 /DB_XREF=gi:10947055 /UG=Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) /FL=gb:NM_020987.1 gb:U13616.1
222209_s_at	-2.75	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRNA /DB_XREF=gi:7020930 /UG=Hs.183887 hypothetical protein FLJ22104
206633_at	-2.75	gb:NM_000079.1 /DEF=Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (CHRNA1), mRNA. /FEA=mRNA /GEN=CHRNA1 /PROD=cholinergic receptor, nicotinic, alphapolypeptide 1 (muscle) precursor /DB_XREF=gi:4557456 /UG=Hs.2266 cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) /FL=gb:NM_000079.1
212307_s_at	-2.75	Consensus includes gb:BF001665 /FEA=EST /DB_XREF=gi:10701940 /DB_XREF=est:7g91d11.x1 /CLONE=IMAGE:3313845 /UG=Hs.100293 O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
215504_x_at	-2.77	Consensus includes gb:AF131777.1 /DEF=Homo sapiens clone 25061 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406602 /UG=Hs.183475 Homo sapiens clone 25061 mRNA sequence
205355_at	-2.77	gb:NM_001609.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, shortbranched chain (ACADSB), nuclear

		gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADSB /PROD=acyl-Coenzyme A dehydrogenase, shortbranchedchain precursor /DB_XREF=gi:4501858 /UG=Hs.81934 acyl-Coenzyme A dehydrogenase, shortbranched chain /FL=gb:NM_001609.1 gb:U12778.1
64900_at	-2.78	Cluster Incl. AA401703:zt60f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-726761 /clone_end=5 /gb=AA401703 /gi=2057294 /ug=Hs.6853 /len=580
219317_at	-2.79	gb:NM_007195.1 /DEF=Homo sapiens polymerase (DNA directed) iota (POLI), mRNA. /FEA=mRNA /GEN=POLI /PROD=polymerase (DNA directed) iota /DB_XREF=gi:6005847 /UG=Hs.271699 polymerase (DNA directed) iota /FL=gb:AL136670.1 gb:AF140501.1 gb:NM_007195.1 gb:AF245438.1
219080_s_at	-2.8	gb:NM_019857.1 /DEF=Homo sapiens CTP synthase II (CTPS2), mRNA. /FEA=mRNA /GEN=CTPS2 /PROD=CTP synthase II /DB_XREF=gi:9789918 /UG=Hs.58553 CTP synthase II /FL=gb:AF226667.1 gb:NM_019857.1
201940_at	-2.8	Consensus includes gb:AA897514 /FEA=EST /DB_XREF=gi:3034134 /DB_XREF=est:aj62b12.s1 /CLONE=IMAGE:1394879 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:D85390.1 gb:NM_001304.2
218736_s_at	-2.8	gb:NM_017734.1 /DEF=Homo sapiens hypothetical protein FLJ20271 (FLJ20271), mRNA. /FEA=mRNA /GEN=FLJ20271 /PROD=hypothetical protein FLJ20271 /DB_XREF=gi:8923242 /UG=Hs.14606 hypothetical protein FLJ20271 /FL=gb:NM_017734.1
215577_at	-2.81	Consensus includes gb:AU146791 /FEA=EST /DB_XREF=gi:11008312 /DB_XREF=est:AU146791 /CLONE=HEMBB1001531 /UG=Hs.287474 Homo sapiens cDNA FLJ12000 fis, clone HEMBB1001531
205569_at	-2.82	gb:NM_014398.1 /DEF=Homo sapiens similar to lysosome-associated membrane glycoprotein (TSC403), mRNA. /FEA=mRNA /GEN=TSC403 /PROD=similar to lysosome-associated membraneglycoprotein /DB_XREF=gi:7657660 /UG=Hs.10887 similar to lysosome-associated membrane glycoprotein /FL=gb:AB013924.1 gb:NM_014398.1
217028_at	-2.82	Consensus includes gb:AJ224869 /DEF=Homo sapiens CXCR4 gene encoding receptor CXCR4 /FEA=mRNA /DB_XREF=gi:3059119 /UG=Hs.89414 chemokine (C-X-C motif), receptor 4 (fusin)
201943_s_at	-2.83	gb:NM_001304.2 /DEF=Homo sapiens carboxypeptidase D (CPD), mRNA. /FEA=mRNA /GEN=CPD /PROD=carboxypeptidase D precursor /DB_XREF=gi:8051580 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:D85390.1 gb:NM_001304.2
213186_at	-2.83	Consensus includes gb:BG502305 /FEA=EST /DB_XREF=gi:13463822 /DB_XREF=est:602550583F1 /CLONE=IMAGE:4657940 /UG=Hs.165662 KIAA0675 gene product
203845_at	-2.83	Consensus includes gb:AV727449 /FEA=EST /DB_XREF=gi:10836870 /DB_XREF=est:AV727449 /CLONE=HTCAYG01 /UG=Hs.199061 p300CBP-associated factor /FL=gb:U57317.2 gb:NM_003884.2
219343_at	-2.84	gb:NM_017913.1 /DEF=Homo sapiens hypothetical protein FLJ20639 (FLJ20639), mRNA. /FEA=mRNA /GEN=FLJ20639 /PROD=hypothetical protein FLJ20639 /DB_XREF=gi:8923591 /UG=Hs.128646 hypothetical protein FLJ20639 /FL=gb:NM_017913.1
218923_at	-2.84	Consensus includes gb:AW304174 /FEA=EST /DB_XREF=gi:6713863 /DB_XREF=est:xv61d01.x1 /CLONE=IMAGE:2817601 /UG=Hs.135578 chitobiase, di-N-acetyl- /FL=gb:M95767.1 gb:NM_004388.1
207463_x_at	-2.86	gb:NM_002771.1 /DEF=Homo sapiens protease, serine, 3 (trypsin 3) (PRSS3), mRNA. /FEA=mRNA /GEN=PRSS3 /PROD=protease, serine, 3 (trypsin 3) /DB_XREF=gi:4506148 /UG=Hs.278310 protease, serine, 3 (trypsin 3) /FL=gb:NM_002771.1
205571_at	-2.86	gb:NM_015929.1 /DEF=Homo sapiens lipoyltransferase (LOC51601), mRNA. /FEA=mRNA /GEN=LOC51601 /PROD=lipoyltransferase /DB_XREF=gi:7706251 /UG=Hs.112356 lipoyltransferase /FL=gb:AB017566.1 gb:NM_015929.1
221841_s_at	-2.89	Consensus includes gb:BF514079 /FEA=EST /DB_XREF=gi:11599258 /DB_XREF=est:UI-H-BW1-amw-b-08-0-UI.s1 /CLONE=IMAGE:3071198 /UG=Hs.7934 Kruppel-like factor 4 (gut)

214373_at	-2.89	Consensus includes gb:AI582773 /FEA=EST /DB_XREF=gi:4568670 /DB_XREF=est:tn17d08.x1 /CLONE=IMAGE:2167887 /UG=Hs.125682 protein phosphatase 4 regulatory subunit 2
205479_s_at	-2.89	gb:NM_002658.1 /DEF=Homo sapiens plasminogen activator, urokinase (PLAU), mRNA. /FEA=mRNA /GEN=PLAU /PROD=plasminogen activator, urokinase /DB_XREF=gi:4505862 /UG=Hs.77274 plasminogen activator, urokinase /FL=gb:M15476.1 gb:NM_002658.1
213359_at	-2.9	Consensus includes gb:W74620 /FEA=EST /DB_XREF=gi:1384833 /DB_XREF=est:zd77e04.s1 /CLONE=IMAGE:346686 /UG=Hs.303627 heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA-binding protein 1, 37kD)
208608_s_at	-2.9	gb:NM_021021.1 /DEF=Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kD, basic component 1) (SNTB1), mRNA. /FEA=CDS /GEN=SNTB1 /PROD=syntrophin, beta 1 (dystrophin-associatedprotein A1, 59kD, basic component 1) /DB_XREF=gi:11321639 /UG=Hs.95011 syntrophin, beta 1 (dystrophin-associated protein A1, 59kD, basic component 1) /FL=gb:NM_021021.1
218087_s_at	-2.9	gb:NM_015385.1 /DEF=Homo sapiens SH3-domain protein 5 (ponsin) (SH3D5), mRNA. /FEA=mRNA /GEN=SH3D5 /PROD=ponsin /DB_XREF=gi:7661699 /UG=Hs.108924 SH3-domain protein 5 (ponsin) /FL=gb:AL117472.1 gb:NM_015385.1
221586_s_at	-2.91	gb:U15642.1 /DEF=Human transcription factor E2F-5 mRNA, complete cds. /FEA=mRNA /PROD=E2F-5 /DB_XREF=gi:758415 /UG=Hs.2331 E2F transcription factor 5, p130-binding /FL=gb:NM_001951.2 gb:U15642.1 gb:U31556.1
215578_at	-2.91	Consensus includes gb:AU145365 /FEA=EST /DB_XREF=gi:11006886 /DB_XREF=est:AU145365 /CLONE=HEMBA1004629 /UG=Hs.287437 Homo sapiens cDNA FLJ11662 fis, clone HEMBA1004629
205633_s_at	-2.92	gb:NM_000688.1 /DEF=Homo sapiens aminolevulinate, delta-, synthase 1 (ALAS1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ALAS1 /PROD=aminolevulinate, delta-, synthase 1 /DB_XREF=gi:4502024 /UG=Hs.78712 aminolevulinate, delta-, synthase 1 /FL=gb:NM_000688.1
212942_s_at	-2.92	Consensus includes gb:AB033025.1 /DEF=Homo sapiens mRNA for KIAA1199 protein, partial cds. /FEA=mRNA /GEN=KIAA1199 /PROD=KIAA1199 protein /DB_XREF=gi:6330400 /UG=Hs.50081 KIAA1199 protein
209114_at	-2.93	gb:AF133425.1 /DEF=Homo sapiens tetraspanin TM4-C mRNA, complete cds. /FEA=mRNA /PROD=tetraspanin TM4-C /DB_XREF=gi:6434903 /UG=Hs.38972 tetraspan 1 /FL=gb:AF054838.1 gb:AF065388.1 gb:NM_005727.1 gb:AF133425.1
202259_s_at	-2.93	gb:NM_014887.1 /DEF=Homo sapiens hypothetical protein from BCRA2 region (CG005), mRNA. /FEA=mRNA /GEN=CG005 /PROD=hypothetical protein from BCRA2 region /DB_XREF=gi:7656970 /UG=Hs.23518 hypothetical protein from BCRA2 region /FL=gb:NM_014887.1
213017_at	-2.94	Consensus includes gb:AL534702 /FEA=EST /DB_XREF=gi:12798195 /DB_XREF=est:AL534702 /CLONE=CS0DF006YN17 (3 prime) /UG=Hs.13377 Homo sapiens clone 23649 and 23755 unknown mRNA, partial cds
202202_s_at	-2.95	gb:NM_002290.2 /DEF=Homo sapiens laminin, alpha 4 (LAMA4), mRNA. /FEA=mRNA /GEN=LAMA4 /PROD=laminin, alpha 4 precursor /DB_XREF=gi:9845494 /UG=Hs.78672 laminin, alpha 4 /FL=gb:NM_002290.2
219880_at	-2.95	gb:NM_022907.1 /DEF=Homo sapiens hypothetical protein FLJ23053 (FLJ23053), mRNA. /FEA=mRNA /GEN=FLJ23053 /PROD=hypothetical protein FLJ23053 /DB_XREF=gi:12597650 /UG=Hs.94037 hypothetical protein FLJ23053 /FL=gb:NM_022907.1
203407_at	-2.95	gb:NM_002705.1 /DEF=Homo sapiens periplakin (PPL), mRNA. /FEA=mRNA /GEN=PPL /PROD=periplakin /DB_XREF=gi:4505992 /UG=Hs.74304 periplakin /FL=gb:AF001691.1 gb:NM_002705.1
200841_s_at	-2.96	Consensus includes gb:AI142677 /FEA=EST /DB_XREF=gi:3659036 /DB_XREF=est:ok33h03.s1 /CLONE=IMAGE:1509653 /UG=Hs.55921 glutamyl-prolyl-tRNA synthetase /FL=gb:NM_004446.1

212459_x_at	-2.96	Consensus includes gb:BF593940 /FEA=EST /DB_XREF=gi:11686264 /DB_XREF=est:nab48f10.x1 /CLONE=IMAGE:3269154 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
216268_s_at	-2.97	Consensus includes gb:U77914.1 /DEF=Human soluble protein Jagged mRNA, partial cds. /FEA=mRNA /PROD=soluble protein Jagged /DB_XREF=gi:1684889 /UG=Hs.91143 jagged 1 (Alagille syndrome)
202454_s_at	-2.97	gb:NM_001982.1 /DEF=Homo sapiens v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 (ERBB3), mRNA. /FEA=mRNA /GEN=ERBB3 /PROD=v-erb-b2 avian erythroblastic leukemia viraloncogene homolog 3 /DB_XREF=gi:4503596 /UG=Hs.199067 v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 /FL=gb:M29366.1 gb:M34309.1 gb:NM_001982.1
203830_at	-2.99	gb:NM_022344.1 /DEF=Homo sapiens protein kinase Njmu-R1 (NJMU-R1), mRNA. /FEA=mRNA /GEN=NJMU-R1 /PROD=protein kinase Njmu-R1 /DB_XREF=gi:11641248 /UG=Hs.9800 protein kinase Njmu-R1 /FL=gb:AF305686.1 gb:NM_022344.1
202769_at	-3	Consensus includes gb:AW134535 /FEA=EST /DB_XREF=gi:6138088 /DB_XREF=est:UI-H-BI1-abv-g-06-0-UI.s1 /CLONE=IMAGE:2713163 /UG=Hs.79069 cyclin G2 /FL=gb:U47414.1 gb:NM_004354.1
205239_at	-3	gb:NM_001657.1 /DEF=Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA. /FEA=mRNA /GEN=AREG /PROD=amphiregulin (schwannoma-derived growth factor) /DB_XREF=gi:4502198 /UG=Hs.270833 amphiregulin (schwannoma-derived growth factor) /FL=gb:M30704.1 gb:NM_001657.1
207563_s_at	-3	gb:U77413.1 /DEF=Human O-linked GlcNAc transferase mRNA, complete cds. /FEA=mRNA /PROD=O-linked GlcNAc transferase /DB_XREF=gi:2266993 /UG=Hs.100293 O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) /FL=gb:U77413.1 gb:NM_003605.2
210078_s_at	-3.02	gb:L39833.1 /DEF=Homo sapiens (clone hKvBeta3) K+ channel beta subunit mRNA, complete cds. /FEA=mRNA /PROD=K+ channel beta-subunit /DB_XREF=gi:666896 /UG=Hs.172471 potassium voltage-gated channel, shaker-related subfamily, beta member 1 /FL=gb:L39833.1 gb:U16953.1
202800_at	-3.02	gb:NM_004172.1 /DEF=Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=SLC1A3 /PROD=solute carrier family 1 (glial high affinityglutamate transporter), member 3 /DB_XREF=gi:4759125 /UG=Hs.75379 solute carrier family 1 (glial high affinity glutamate transporter), member 3 /FL=gb:D26443.1 gb:NM_004172.1 gb:U03504.1
203763_at	-3.03	gb:NM_016008.1 /DEF=Homo sapiens CGI-60 protein (LOC51626), mRNA. /FEA=mRNA /GEN=LOC51626 /PROD=CGI-60 protein /DB_XREF=gi:7706299 /UG=Hs.7627 CGI-60 protein /FL=gb:AF151818.1 gb:NM_016008.1
207761_s_at	-3.04	gb:NM_014033.1 /DEF=Homo sapiens DKFZP586A0522 protein (DKFZP586A0522), mRNA. /FEA=mRNA /GEN=DKFZP586A0522 /PROD=DKFZP586A0522 protein /DB_XREF=gi:13378140 /UG=Hs.288771 DKFZP586A0522 protein /FL=gb:NM_014033.1
214835_s_at	-3.04	Consensus includes gb:AF131748.1 /DEF=Homo sapiens clone 25191 GTP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA sequence, partial cds. /FEA=mRNA /PROD=GTP-specific succinyl-CoA synthetase betasubunit /DB_XREF=gi:4406563 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
207604_s_at	-3.04	gb:NM_003615.1 /DEF=Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA. /FEA=mRNA /GEN=SLC4A7 /PROD=solute carrier family 4, sodium bicarbonatecotransporter, member 7 /DB_XREF=gi:4507028 /UG=Hs.132904 solute carrier family 4, sodium bicarbonate cotransporter, member 7 /FL=gb:AB012130.1 gb:NM_003615.1
206043_s_at	-3.05	gb:NM_014861.1 /DEF=Homo sapiens KIAA0703 gene product (KIAA0703), mRNA. /FEA=mRNA /GEN=KIAA0703 /PROD=KIAA0703 gene product /DB_XREF=gi:7662255 /UG=Hs.6168 KIAA0703 gene product /FL=gb:AB014603.1 gb:NM_014861.1

204485_s_at	-3.06	gb:NM_005486.1 /DEF=Homo sapiens target of myb1 (chicken) homolog-like 1 (TOM1L1), mRNA. /FEA=mRNA /GEN=TOM1L1 /PROD=target of myb1 (chicken) homolog-like 1 /DB_XREF=gi:4885638 /UG=Hs.153504 target of myb1 (chicken) homolog-like 1 /FL=gb:NM_005486.1
203779_s_at	-3.06	gb:NM_005797.1 /DEF=Homo sapiens epithelial V-like antigen 1 (EVA1), mRNA. /FEA=mRNA /GEN=EVA1 /PROD=epithelial V-like antigen 1 precursor /DB_XREF=gi:5032246 /UG=Hs.116651 epithelial V-like antigen 1 /FL=gb:AF304447.1 gb:AF030455.1 gb:NM_005797.1 gb:AF275945.1
219388_at	-3.08	gb:NM_024915.1 /DEF=Homo sapiens hypothetical protein FLJ13782 (FLJ13782), mRNA. /FEA=mRNA /GEN=FLJ13782 /PROD=hypothetical protein FLJ13782 /DB_XREF=gi:13376381 /UG=Hs.257924 hypothetical protein FLJ13782 /FL=gb:NM_024915.1
210306_at	-3.08	gb:U89358.1 /DEF=Human l(3)mbt protein homolog mRNA, complete cds. /FEA=mRNA /PROD=l(3)mbt protein homolog /DB_XREF=gi:3811110 /UG=Hs.300863 lethal (3) malignant brain tumor l(3)mbt protein (Drosophila) homolog /FL=gb:U89358.1
209209_s_at	-3.08	Consensus includes gb:AW469573 /FEA=EST /DB_XREF=gi:7039679 /DB_XREF=est:hd29e09.x1 /CLONE=IMAGE:2910952 /UG=Hs.75260 mitogen inducible 2 /FL=gb:Z24725.1
205842_s_at	-3.1	gb:AF001362.1 /DEF=Homo sapiens Jak2 kinase (JAK2) mRNA, complete cds. /FEA=mRNA /GEN=JAK2 /PROD=Jak2 kinase /DB_XREF=gi:3236321 /UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) /FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
205229_s_at	-3.11	Consensus includes gb:AA669336 /FEA=EST /DB_XREF=gi:2630835 /DB_XREF=est:ad47a02.s1 /CLONE=IMAGE:884810 /UG=Hs.21016 coagulation factor C (Limulus polyphemus) homology (cochlin) /FL=gb:AF006740.1 gb:NM_004086.1
214437_s_at	-3.13	Consensus includes gb:NM_005412.1 /DEF=Homo sapiens serine hydroxymethyltransferase 2 (mitochondrial) (SHMT2), mRNA. /FEA=CDS /GEN=SHMT2 /PROD=serine hydroxymethyltransferase 2(mitochondrial) /DB_XREF=gi:4885594 /UG=Hs.75069 serine hydroxymethyltransferase 2 (mitochondrial) /FL=gb:NM_005412.1
205808_at	-3.14	gb:NM_004318.1 /DEF=Homo sapiens aspartate beta-hydroxylase (ASPH), mRNA. /FEA=mRNA /GEN=ASPH /PROD=aspartate beta-hydroxylase /DB_XREF=gi:4757799 /UG=Hs.283664 aspartate beta-hydroxylase /FL=gb:U03109.1 gb:NM_004318.1
209122_at	-3.19	gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, complete cds. /FEA=mRNA /PROD=adipose differentiation-related protein /DB_XREF=gi:13477306 /UG=Hs.3416 adipose differentiation-related protein /FL=gb:BC005127.1 gb:NM_001122.1
218858_at	-3.21	gb:NM_022783.1 /DEF=Homo sapiens hypothetical protein FLJ12428 (FLJ12428), mRNA. /FEA=mRNA /GEN=FLJ12428 /PROD=hypothetical protein FLJ12428 /DB_XREF=gi:12232472 /UG=Hs.87729 hypothetical protein FLJ12428 /FL=gb:AL136678.1 gb:NM_022783.1
209884_s_at	-3.21	gb:AF047033.1 /DEF=Homo sapiens sodium bicarbonate cotransporter 3 (SLC4A7) mRNA, complete cds. /FEA=mRNA /GEN=SLC4A7 /PROD=sodium bicarbonate cotransporter 3 /DB_XREF=gi:5051627 /UG=Hs.132904 solute carrier family 4, sodium bicarbonate cotransporter, member 7 /FL=gb:AF047033.1
221899_at	-3.24	Consensus includes gb:AI809961 /FEA=EST /DB_XREF=gi:5396527 /DB_XREF=est:wf64b09.x1 /CLONE=IMAGE:2360345 /UG=Hs.23518 hypothetical protein from BCRA2 region
215772_x_at	-3.25	Consensus includes gb:AL050226.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586M2023 (from clone DKFZp586M2023); partial cds. /FEA=mRNA /GEN=DKFZp586M2023 /PROD=hypothetical protein /DB_XREF=gi:4884469 /UG=Hs.247309 succinate-CoA ligase, GDP-forming, beta subunit
221218_s_at	-3.25	gb:NM_022445.1 /DEF=Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA. /FEA=mRNA /GEN=TPK1 /PROD=mouse thiamin pyrophosphokinase homolog /DB_XREF=gi:11990617 /UG=Hs.58715 thiamine pyrophosphokinase /FL=gb:NM_022445.1

219443_at	-3.25	gb:NM_017714.1 /DEF=Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA. /FEA=mRNA /GEN=FLJ20212 /PROD=hypothetical protein FLJ20212 /DB_XREF=gi:8923201 /UG=Hs.88367 hypothetical protein FLJ20212 /FL=gb:NM_017714.1
209131_s_at	-3.3	gb:U55936.1 /DEF=Human SNAP-23 mRNA, complete cds. /FEA=mRNA /PROD=SNAP-23 /DB_XREF=gi:1374812 /UG=Hs.184376 synaptosomal-associated protein, 23kD /FL=gb:BC000148.2 gb:BC003686.1 gb:U55936.1 gb:Y09567.1
202887_s_at	-3.31	gb:NM_019058.1 /DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. /FEA=mRNA /GEN=FLJ20500 /PROD=hypothetical protein /DB_XREF=gi:9506686 /UG=Hs.111244 hypothetical protein /FL=gb:AL136668.1 gb:NM_019058.1
203817_at	-3.31	Consensus includes gb:W93728 /FEA=EST /DB_XREF=gi:1422918 /DB_XREF=est:zd96a11.s1 /CLONE=IMAGE:357308 /UG=Hs.77890 guanylate cyclase 1, soluble, beta 3 /FL=gb:NM_000857.1
91826_at	-3.35	Cluster Incl. AI219073:qg16e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1759718 /clone_end=3 /gb=AI219073 /gi=3801276 /ug=Hs.126062 /len=555
201942_s_at	-3.35	gb:D85390.1 /DEF=Homo sapiens mRNA for gp180-carboxypeptidase D-like enzyme, complete cds. /FEA=mRNA /PROD=gp180-carboxypeptidase D-like enzyme /DB_XREF=gi:3641620 /UG=Hs.5057 carboxypeptidase D /FL=gb:U65090.1 gb:D85390.1 gb:NM_001304.2
219014_at	-3.37	gb:NM_016619.1 /DEF=Homo sapiens hypothetical protein (LOC51316), mRNA. /FEA=mRNA /GEN=LOC51316 /PROD=hypothetical protein /DB_XREF=gi:7706157 /UG=Hs.107139 hypothetical protein /FL=gb:AF208846.1 gb:NM_016619.1
204199_at	-3.39	gb:NM_014636.1 /DEF=Homo sapiens Ral guanine nucleotide exchange factor RalGPS1A (RalGPS1A), mRNA. /FEA=mRNA /GEN=RalGPS1A /PROD=Ral guanine nucleotide exchange factor RalGPS1A /DB_XREF=gi:7662069 /UG=Hs.170307 Ral guanine nucleotide exchange factor RalGPS1A /FL=gb:AB002349.1 gb:NM_014636.1
210377_at	-3.42	gb:D16350.1 /DEF=Human SA mRNA for SA gene product, complete cds. /FEA=mRNA /GEN=SA /DB_XREF=gi:471131 /UG=Hs.181345 SA (rat hypertension-associated) homolog /FL=gb:D16350.1
215203_at	-3.43	Consensus includes gb:AW438464 /FEA=EST /DB_XREF=gi:6973770 /DB_XREF=est:xu43g07.x1 /CLONE=IMAGE:2804508 /UG=Hs.288760 Homo sapiens cDNA FLJ12327 fis, clone MAMMA1002140
201131_s_at	-3.44	gb:NM_004360.1 /DEF=Homo sapiens cadherin 1, type 1, E-cadherin (epithelial) (CDH1), mRNA. /FEA=mRNA /GEN=CDH1 /PROD=cadherin 1, type 1, E-cadherin (epithelial) /DB_XREF=gi:4757959 /UG=Hs.194657 cadherin 1, type 1, E-cadherin (epithelial) /FL=gb:L08599.1 gb:NM_004360.1
222358_x_at	-3.44	Consensus includes gb:AI523613 /FEA=EST /DB_XREF=gi:4437748 /DB_XREF=est:tg95a07.x1 /CLONE=IMAGE:2116500 /UG=Hs.293495 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
214705_at	-3.44	Consensus includes gb:AJ001306.1 /DEF=Homo sapiens mRNA for PDZ domain protein. /FEA=mRNA /PROD=PDZ domain protein /DB_XREF=gi:2370148 /UG=Hs.321197 PDZ domain protein (Drosophila inaD-like)
206548_at	-3.44	gb:NM_024880.1 /DEF=Homo sapiens hypothetical protein FLJ23556 (FLJ23556), mRNA. /FEA=mRNA /GEN=FLJ23556 /PROD=hypothetical protein FLJ23556 /DB_XREF=gi:13376321 /UG=Hs.214039 hypothetical protein FLJ23556 /FL=gb:NM_024880.1
205841_at	-3.47	gb:NM_004972.2 /DEF=Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA. /FEA=mRNA /GEN=JAK2 /PROD=Janus kinase 2 /DB_XREF=gi:13325062 /UG=Hs.115541 Janus kinase 2 (a protein tyrosine kinase) /FL=gb:NM_004972.2 gb:AF005216.1 gb:AF058925.1 gb:AF001362.1
219115_s_at	-3.48	gb:NM_014432.1 /DEF=Homo sapiens interleukin 20 receptor, alpha (IL20RA), mRNA. /FEA=mRNA /GEN=IL20RA /PROD=interleukin 20 receptor, alpha /DB_XREF=gi:7657690 /UG=Hs.21814 interleukin 20 receptor, alpha

		/FL=gb:AF184971.1 gb:NM_014432.1
203896_s_at	-3.49	gb:NM_000933.1 /DEF=Homo sapiens phospholipase C, beta 4 (PLCB4), mRNA. /FEA=mRNA /GEN=PLCB4 /PROD=phospholipase C, beta 4 /DB_XREF=gi:4505866 /UG=Hs.283006 phospholipase C, beta 4 /FL=gb:NM_000933.1 gb:L41349.1
209498_at	-3.5	Consensus includes gb:X16354.1 /DEF=Human mRNA for transmembrane carcinoembryonic antigen BGPa (formerly TM1-CEA). /FEA=mRNA /PROD=TM1-CEA preprotein /DB_XREF=gi:37197 /UG=Hs.50964 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) /FL=gb:J03858.1
212406_s_at	-3.52	Consensus includes gb:AB028973.1 /DEF=Homo sapiens mRNA for KIAA1050 protein, partial cds. /FEA=mRNA /GEN=KIAA1050 /PROD=KIAA1050 protein /DB_XREF=gi:5689436 /UG=Hs.184628 hypothetical protein FLJ10883
218677_at	-3.53	gb:NM_020672.1 /DEF=Homo sapiens S100-type calcium binding protein A14 (LOC57402), mRNA. /FEA=mRNA /GEN=LOC57402 /PROD=S100-type calcium binding protein A14 /DB_XREF=gi:10190711 /UG=Hs.288998 S100-type calcium binding protein A14 /FL=gb:NM_020672.1 gb:BC005019.1 gb:AY007220.1
215314_at	-3.54	Consensus includes gb:AU146646 /FEA=EST /DB_XREF=gi:11008167 /DB_XREF=est:AU146646 /CLONE=HEMBB1001096 /UG=Hs.179752 Homo sapiens cDNA FLJ10270 fis, clone HEMBB1001096
214823_at	-3.58	Consensus includes gb:AF033199.1 /DEF=Homo sapiens C2H2 zinc finger protein pseudogene, mRNA sequence. /FEA=mRNA /DB_XREF=gi:3252864 /UG=Hs.8198 zinc finger protein 204
220622_at	-3.6	gb:NM_024727.1 /DEF=Homo sapiens hypothetical protein FLJ23259 (FLJ23259), mRNA. /FEA=mRNA /GEN=FLJ23259 /PROD=hypothetical protein FLJ23259 /DB_XREF=gi:13376039 /UG=Hs.114005 hypothetical protein FLJ23259 /FL=gb:NM_024727.1
217513_at	-3.62	Consensus includes gb:BG334495 /FEA=EST /DB_XREF=gi:13140933 /DB_XREF=est:602461128F1 /CLONE=IMAGE:4577718 /UG=Hs.228201 ESTs, Moderately similar to AF118094 25 PRO1992 H.sapiens
203509_at	-3.64	gb:NM_003105.2 /DEF=Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA. /FEA=mRNA /GEN=SORL1 /PROD=sortilin-related receptor, L(DLR class) Arepeats-containing /DB_XREF=gi:6325473 /UG=Hs.278571 sortilin-related receptor, L(DLR class) A repeats-containing /FL=gb:U60975.2 gb:NM_003105.2
218839_at	-3.7	gb:NM_012258.1 /DEF=Homo sapiens hairyenhancer-of-split related with YRPW motif 1 (HEY1), mRNA. /FEA=mRNA /GEN=HEY1 /PROD=hairyenhancer-of-split related with YRPW motif1 /DB_XREF=gi:6912411 /UG=Hs.234434 hairyenhancer-of-split related with YRPW motif 1 /FL=gb:AF311883.1 gb:BC001873.1 gb:AF151522.1 gb:AF176422.1 gb:NM_012258.1 gb:AF232239.1
205500_at	-3.72	gb:NM_001735.1 /DEF=Homo sapiens complement component 5 (C5), mRNA. /FEA=mRNA /GEN=C5 /PROD=complement component 5 /DB_XREF=gi:4502506 /UG=Hs.1281 complement component 5 /FL=gb:M57729.1 gb:NM_001735.1
221827_at	-3.73	Consensus includes gb:BE788439 /FEA=EST /DB_XREF=gi:10209637 /DB_XREF=est:601475616F1 /CLONE=IMAGE:3878643 /UG=Hs.247280 HBV associated factor
218976_at	-3.73	gb:NM_021800.1 /DEF=Homo sapiens J domain containing protein 1 (JDP1), mRNA. /FEA=mRNA /GEN=JDP1 /PROD=J domain containing protein 1 /DB_XREF=gi:11141870 /UG=Hs.260720 J domain containing protein 1 /FL=gb:NM_021800.1 gb:AF176012.1
207781_s_at	-3.75	gb:NM_021998.1 /DEF=Homo sapiens zinc finger protein 6 (CMPX1) (ZNF6), mRNA. /FEA=mRNA /GEN=ZNF6 /PROD=zinc finger protein 6 (CMPX1) /DB_XREF=gi:11527399 /UG=Hs.323950 zinc finger protein 6 (CMPX1) /FL=gb:NM_021998.1
211559_s_at	-3.81	gb:L49506.1 /DEF=Homo sapiens cyclin G2 mRNA, complete cds. /FEA=mRNA /PROD=cyclin G2 /DB_XREF=gi:1236234 /UG=Hs.79069 cyclin G2 /FL=gb:L49506.1

44783_s_at	-3.81	Cluster Incl. R61374:yh15e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-37665 /clone_end=3 /gb=R61374 /gi=832069 /ug=Hs.234434 /len=434
208161_s_at	-3.82	gb:NM_020037.1 /DEF=Homo sapiens ATP-binding cassette, sub-family C (CFTRMRP), member 3 (ABCC3), transcript variant MRP3A, mRNA. /FEA=mRNA /GEN=ABCC3 /PROD=ATP-binding cassette, sub-family C, member 3,isoform MRP3A /DB_XREF=gi:9955971 /UG=Hs.90786 ATP-binding cassette, sub-family C (CFTRMRP), member 3 /FL=gb:AF085691.1 gb:NM_020037.1
205968_at	-3.84	gb:NM_002252.1 /DEF=Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /FEA=mRNA /GEN=KCNS3 /PROD=potassium voltage-gated channel,delayed-rectifier, subfamily S, member 3 /DB_XREF=gi:4504862 /UG=Hs.47584 potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 /FL=gb:BC004148.1 gb:BC004987.1 gb:AF043472.1 gb:NM_002252.1
218145_at	-3.85	gb:NM_021158.1 /DEF=Homo sapiens protein kinase domains containing protein similar to phosphoprotein C8FW (LOC57761), mRNA. /FEA=mRNA /GEN=LOC57761 /PROD=protein kinase domains containing proteinsimilar to phosphoprotein C8FW /DB_XREF=gi:11056039 /UG=Hs.26802 protein kinase domains containing protein similar to phosphoprotein C8FW /FL=gb:NM_021158.1
221698_s_at	-3.85	gb:AF313468.1 /DEF=Homo sapiens dendritic cell-associated C-type lectin-1 mRNA, complete cds. /FEA=mRNA /PROD=dendritic cell-associated C-type lectin-1 /DB_XREF=gi:13649707 /FL=gb:AF313468.1
215250_at	-3.86	Consensus includes gb:AU147317 /FEA=EST /DB_XREF=gi:11008838 /DB_XREF=est:AU147317 /CLONE=MAMMA1000340 /UG=Hs.287491 Homo sapiens cDNA FLJ12140 fis, clone MAMMA1000340
211668_s_at	-3.87	gb:K03226.1 /DEF=Human preprourokinase mRNA, complete cds. /FEA=mRNA /GEN=PLAU /DB_XREF=gi:340155 /FL=gb:K03226.1
220484_at	-3.88	gb:NM_018298.1 /DEF=Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA. /FEA=mRNA /GEN=FLJ11006 /PROD=hypothetical protein FLJ11006 /DB_XREF=gi:8922819 /UG=Hs.49344 hypothetical protein FLJ11006 /FL=gb:NM_018298.1
206546_at	-3.9	gb:NM_014258.1 /DEF=Homo sapiens synaptonemal complex protein 2 (SYCP2), mRNA. /FEA=mRNA /GEN=SYCP2 /PROD=synaptonemal complex protein 2 /DB_XREF=gi:7657634 /UG=Hs.202676 synaptonemal complex protein 2 /FL=gb:NM_014258.1
205583_s_at	-3.9	gb:NM_024810.1 /DEF=Homo sapiens hypothetical protein FLJ23018 (FLJ23018), mRNA. /FEA=mRNA /GEN=FLJ23018 /PROD=hypothetical protein FLJ23018 /DB_XREF=gi:13376194 /UG=Hs.169078 hypothetical protein FLJ23018 /FL=gb:NM_024810.1
204466_s_at	-3.9	Consensus includes gb:BG260394 /FEA=EST /DB_XREF=gi:12770210 /DB_XREF=est:602371523F1 /CLONE=IMAGE:4479556 /UG=Hs.76930 synuclein, alpha (non A4 component of amyloid precursor) /FL=gb:L08850.1 gb:NM_000345.2
204389_at	-3.91	gb:NM_000240.1 /DEF=Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MAOA /PROD=monoamine oxidase A /DB_XREF=gi:4557734 /UG=Hs.183109 monoamine oxidase A /FL=gb:M68840.1 gb:M69226.1 gb:NM_000240.1
215392_at	-3.95	Consensus includes gb:AU148154 /FEA=EST /DB_XREF=gi:11009675 /DB_XREF=est:AU148154 /CLONE=MAMMA1002744 /UG=Hs.298014 Homo sapiens cDNA FLJ14136 fis, clone MAMMA1002744
205376_at	-4	gb:NM_003866.1 /DEF=Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kD (INPP4B), mRNA. /FEA=mRNA /GEN=INPP4B /PROD=inositol polyphosphate-4-phosphatase, type II,105kD /DB_XREF=gi:4504706 /UG=Hs.153687 inositol polyphosphate-4-phosphatase, type II, 105kD /FL=gb:U96922.1 gb:NM_003866.1
204268_at	-4.04	gb:NM_005978.2 /DEF=Homo sapiens S100 calcium-binding protein A2 (S100A2), mRNA. /FEA=mRNA /GEN=S100A2 /PROD=S100 calcium-binding protein A2 /DB_XREF=gi:9845513 /UG=Hs.38991 S100 calcium-binding protein A2 /FL=gb:BC002829.1 gb:NM_005978.2

211429_s_at	-4.05	gb:AF119873.1 /DEF=Homo sapiens PRO2275 mRNA, complete cds. /FEA=mRNA /PROD=PRO2275 /DB_XREF=gi:7770182 /UG=Hs.297681 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 /FL=gb:AF119873.1
214790_at	-4.05	Consensus includes gb:AK001406.1 /DEF=Homo sapiens cDNA FLJ10544 fis, clone NT2RP2001601, highly similar to Homo sapiens mRNA for KIAA0797 protein. /FEA=mRNA /DB_XREF=gi:7022642 /UG=Hs.27197 SUMO-1-specific protease
205769_at	-4.07	gb:NM_003645.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1), mRNA. /FEA=mRNA /GEN=FACVL1 /PROD=very long-chain fatty-acid-Coenzyme A ligase 1 /DB_XREF=gi:4503652 /UG=Hs.11729 fatty-acid-Coenzyme A ligase, very long-chain 1 /FL=gb:D88308.1 gb:AF096290.1 gb:NM_003645.1
216129_at	-4.11	Consensus includes gb:AL117659.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586I0624 (from clone DKFZp586I0624). /FEA=mRNA /DB_XREF=gi:5912252 /UG=Hs.306353 Homo sapiens mRNA; cDNA DKFZp586I0624 (from clone DKFZp586I0624)
202770_s_at	-4.19	gb:NM_004354.1 /DEF=Homo sapiens cyclin G2 (CCNG2), mRNA. /FEA=mRNA /GEN=CCNG2 /PROD=cyclin G2 /DB_XREF=gi:4757935 /UG=Hs.79069 cyclin G2 /FL=gb:U47414.1 gb:NM_004354.1
210652_s_at	-4.24	gb:BC004399.1 /DEF=Homo sapiens, clone MGC:10985, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10985) /DB_XREF=gi:13325163 /UG=Hs.125783 DEME-6 protein /FL=gb:BC004399.1
208966_x_at	-4.24	gb:AF208043.1 /DEF=Homo sapiens IFI16b (IFI16b) mRNA, complete cds. /FEA=mRNA /GEN=IFI16b /PROD=IFI16b /DB_XREF=gi:6644296 /UG=Hs.155530 interferon, gamma-inducible protein 16 /FL=gb:AF208043.1
207078_at	-4.3	gb:NM_005466.1 /DEF=Homo sapiens RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of) (MED6), mRNA. /FEA=mRNA /GEN=MED6 /PROD=RNA polymerase II transcriptional regulationmediator (Med6, S. cerevisiae, homolog of) /DB_XREF=gi:4885480 /UG=Hs.167738 RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of) /FL=gb:U78082.1 gb:NM_005466.1
202847_at	-4.35	gb:NM_004563.1 /DEF=Homo sapiens phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), mRNA. /FEA=mRNA /GEN=PCK2 /PROD=phosphoenolpyruvate carboxykinase 2(mitochondrial) /DB_XREF=gi:4758885 /UG=Hs.75812 phosphoenolpyruvate carboxykinase 2 (mitochondrial) /FL=gb:BC001454.1 gb:NM_004563.1
219734_at	-4.36	gb:NM_017699.1 /DEF=Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA. /FEA=mRNA /GEN=FLJ20174 /PROD=hypothetical protein FLJ20174 /DB_XREF=gi:8923170 /UG=Hs.114556 hypothetical protein FLJ20174 /FL=gb:NM_017699.1
205009_at	-4.36	gb:NM_003225.1 /DEF=Homo sapiens trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in) (TFF1), mRNA. /FEA=mRNA /GEN=TFF1 /PROD=trefoil factor 1 (breast cancer,estrogen-inducible sequence expressed in) /DB_XREF=gi:4507450 /UG=Hs.1406 trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in) /FL=gb:NM_003225.1
211094_s_at	-4.41	gb:D12625.1 /DEF=Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds. /FEA=mRNA /GEN=NF1 /PROD=NF1 protein isoform /DB_XREF=gi:219939 /UG=Hs.93207 neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) /FL=gb:D12625.1
213307_at	-4.44	Consensus includes gb:AF131790.1 /DEF=Homo sapiens clone 24903 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406618 /UG=Hs.12696 cortactin SH3 domain-binding protein
204734_at	-4.45	gb:NM_002275.1 /DEF=Homo sapiens keratin 15 (KRT15), mRNA. /FEA=mRNA /GEN=KRT15 /PROD=keratin 15 /DB_XREF=gi:4504914 /UG=Hs.80342 keratin 15 /FL=gb:BC002641.1 gb:NM_002275.1
214078_at	-4.48	Consensus includes gb:AF070581.1 /DEF=Homo sapiens clone 24540 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3387953 /UG=Hs.153529 Homo sapiens clone 24540 mRNA sequence

204019_s_at	-4.52	gb:NM_015677.1 /DEF=Homo sapiens hypothetical protein (DKFZP586F1318), mRNA. /FEA=mRNA /GEN=DKFZP586F1318 /PROD=hypothetical protein /DB_XREF=gi:7661669 /UG=Hs.25213 hypothetical protein /FL=gb:NM_015677.1
204891_s_at	-4.53	gb:NM_005356.1 /DEF=Homo sapiens lymphocyte-specific protein tyrosine kinase (LCK), mRNA. /FEA=mRNA /GEN=LCK /PROD=lymphocyte-specific protein tyrosine kinase /DB_XREF=gi:4885448 /UG=Hs.1765 lymphocyte-specific protein tyrosine kinase /FL=gb:M36881.1 gb:U07236.1 gb:NM_005356.1
205576_at	-4.54	gb:NM_000185.2 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1 (SERPIND1), mRNA. /FEA=mRNA /GEN=SERPIND1 /PROD=heparin cofactor II precursor /DB_XREF=gi:7262380 /UG=Hs.1478 serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1 /FL=gb:M12849.1 gb:NM_000185.2
218983_at	-4.56	gb:NM_016546.1 /DEF=Homo sapiens complement C1r-like proteinase precursor, (LOC51279), mRNA. /FEA=mRNA /GEN=LOC51279 /PROD=complement C1r-like proteinase precursor, /DB_XREF=gi:7706082 /UG=Hs.98571 complement C1r-like proteinase precursor, /FL=gb:AF178985.1 gb:NM_016546.1
217678_at	-4.68	Consensus includes gb:AA488687 /FEA=EST /DB_XREF=gi:2216118 /DB_XREF=est:ab38f03.s1 /CLONE=IMAGE:843101 /UG=Hs.284235 ESTs
214753_at	-4.7	Consensus includes gb:AW084068 /FEA=EST /DB_XREF=gi:6039220 /DB_XREF=est:xc26c06.x1 /CLONE=IMAGE:2585386 /UG=Hs.110630 Human BRCA2 region, mRNA sequence CG006
219288_at	-4.81	gb:NM_020685.1 /DEF=Homo sapiens HT021 (HT021), mRNA. /FEA=mRNA /GEN=HT021 /PROD=HT021 /DB_XREF=gi:10190735 /UG=Hs.47166 HT021 /FL=gb:NM_020685.1 gb:AF236158.1
220892_s_at	-4.88	gb:NM_021154.1 /DEF=Homo sapiens phosphoserine aminotransferase (PSA), mRNA. /FEA=mRNA /GEN=PSA /PROD=phosphoserine aminotransferase /DB_XREF=gi:10863954 /UG=Hs.286049 phosphoserine aminotransferase /FL=gb:NM_021154.1 gb:AF113132.1
215123_at	-4.99	Consensus includes gb:AL049250.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D113 (from clone DKFZp564D113). /FEA=mRNA /DB_XREF=gi:4499989 /UG=Hs.194637 BANP homolog, SMAR1 homolog
220518_at	-5.02	gb:NM_024801.1 /DEF=Homo sapiens hypothetical protein FLJ21551 (FLJ21551), mRNA. /FEA=mRNA /GEN=FLJ21551 /PROD=hypothetical protein FLJ21551 /DB_XREF=gi:13376176 /UG=Hs.159231 hypothetical protein FLJ21551 /FL=gb:NM_024801.1
204086_at	-5.06	gb:NM_006115.1 /DEF=Homo sapiens preferentially expressed antigen in melanoma (PRAME), mRNA. /FEA=mRNA /GEN=PRAME /PROD=preferentially expressed antigen of melanoma /DB_XREF=gi:5174640 /UG=Hs.30743 preferentially expressed antigen in melanoma /FL=gb:U65011.1 gb:NM_006115.1
212816_s_at	-5.16	Consensus includes gb:BE613178 /FEA=EST /DB_XREF=gi:9894775 /DB_XREF=est:601452166T1 /CLONE=IMAGE:3855712 /UG=Hs.84152 cystathionine-beta-synthase
209921_at	-5.19	gb:AB040875.1 /DEF=Homo sapiens hxCT mRNA for cystineglutamate exchanger, complete cds. /FEA=mRNA /GEN=hxCT /PROD=cystineglutamate exchanger /DB_XREF=gi:13516845 /UG=Hs.6682 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 /FL=gb:AB040875.1
215717_s_at	-5.31	Consensus includes gb:X62009.1 /DEF=Homo sapiens partial mRNA for fibrillin 5. /FEA=mRNA /PROD=fibrillin 5 /DB_XREF=gi:31399 /UG=Hs.79432 fibrillin 2 (congenital contractural arachnodactyly)
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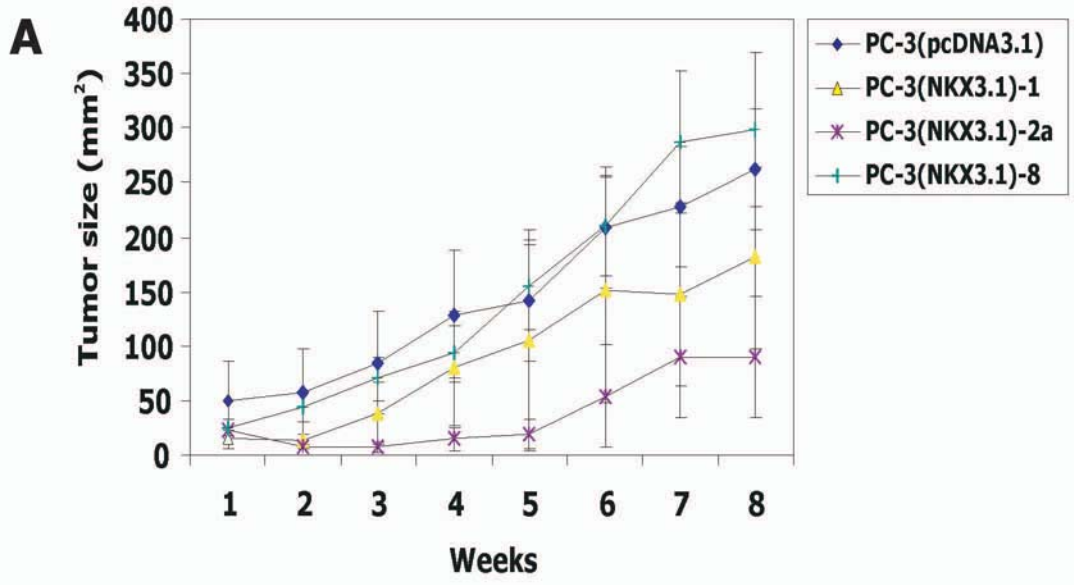
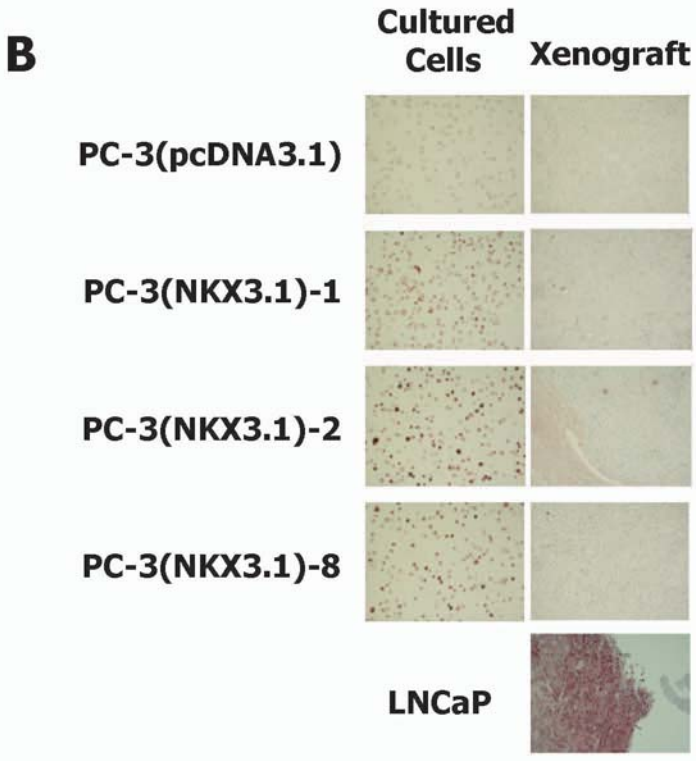
Supplementary Figure 1

Tumor formation by PC-3 derivative cell xenografts. A. PC-3 cells and derivative lines were grown to 80% confluence in a Hyperflask under tissue culture conditions in IMEM containing 10% FBS and 1.2mg/ml G418, trypsinized, and resuspended in IMEM containing 10% FBS to deactivate trypsin. Following two additional washes in cold PBS, a solution of $3x10^6$ cells/100μl PBS were inoculated into the ventral surface of 5 week old female NCr-nude mice and tumors (n=20) were measured in two dimensions once a week for eight weeks. The graph shows average size of PC-3 cell tumors with standard deviations. Tumors were resected at 8 weeks and analyzed by immunohistochemistry. B. Immunohistochemical analysis of derivative PC-3 cell lines for NKX3.1 expression Cultured PC-3 cells were embedded in 1% agarose before paraffin-embedding, sectioning, and staining. Tumor xenografts were dissected at 8 weeks post-inoculation and immediately immersed in 10% buffered formalin before paraffin embedding, sectioning and staining. Slides were microwaved for 5 minutes and immersed in two washes of xylene, followed by successive washes in 100%, 90%, and 70% ethanol, followed by a 5 minute wash in PBS. Slides were steamed in 10mM citrate buffer before being incubated in blocking buffer and NKX3.1 primary antibody solution, followed by application of Biotin-anti-mouse secondary antibody solution. The Vectastain Elite ABC and Vector VIP substrate kits were used for immunohistochemical staining. Slides were visualized with a Zeiss Axioplan-2 microscope and photographs were taken with a Nikon Coolpix 5000 digital camera. On the left are panels with photomicrographs of cultured cells with nuclear expression of NKX3.1. On the right are the respective tumor

xenografts at 8 weeks. As a positive control for expression of NKX3.1 in a xenograft an LNCaP tumor is shown at the bottom.





Muhlbradt
Supplementary Fig 1

Variant NKX3.1 and Serum IGF-1 – Investigation of Interaction in Prostate Cancer

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Abstract

NKX3.1 is a homeobox gene that codes for a haploinsufficient prostate tumor suppressor. NKX3.1 is down regulated in the majority of early prostate cancers resulting in decreased tumor suppression. In cultured cells NKX3.1 suppresses cell growth in part by inducing IGFBP-3 and inhibiting IGF-1 signaling. A SNP (rs2228013) that represents a polymorphic *NKX3.1*(C154T) and codes for a variant protein NKX3.1(R52C) is present in 10% of the population. The *NKX3.1* polymorphism is related to prostatic enlargement and is a minor risk factor for prostate cancer. In this report we expand our analysis of *NKX3.1*(C154T) to two populations. We investigated further the role of rs2228013 in prostate cancer risk for 937 prostate cancer cases and 1086 age-matched controls from a nested case-control study within the prospective Physicians' Health Study (Massachusetts, USA) (PHS) and among 798 cases and 527 controls retrospectively collected in the Risk Factors for Prostate Cancer Study of the Victoria Cancer Council (Australia) (RFPCS). In the PHS we found no overall association between carrying the variant T allele in rs2228013 in *NKX3.1* and prostate cancer risk (OR=1.25, 0.92 -1.71) relative to men with the homozygous C genotype. A subgroup analysis for cases diagnosed before age 70 showed an increased risk (RR=1.55; 95%CI: 1.04-2.31) of overall prostate cancer. In this age-group the risk of metastatic cancer at diagnosis or of fatal cancer was even higher in carriers of the T allele (RR=2.15; 95%CI: 1.00-4.63). These associations were not replicated in the RFPCS. Serum IGF-I levels were found to be a risk factor for prostate cancer in both study populations. IGFBP-3 is a known inhibitor of IGF-I signaling. The wild type NKX3.1 protein can induced IGFBP-3 expression *in vitro* but the variant NKX3.1(R52C) protein cannot. Because of the association *in vitro* between NKX3.1 and IGFBP-3 expression and IGF-I signaling, we investigated the interaction between serum IGF-I level, a known risk factor for prostate cancer, and *NKX3.1* genotype in the populations from PHS and RFPCS.

We report that *NKX3.1* genotype does not modify the association between serum IGF-I levels and prostate cancer risk.

Adenocarcinoma of the prostate, like many epithelial malignancies, initiates in epithelial cells that acquire the precursor or gatekeeper mutations required for development of the malignant phenotype. In the majority of early prostate cancers a region of 8p21.2 is lost resulting in loss of the homeobox gene *NKX3.1* that is expressed specifically in prostate luminal epithelial cells (1-3). Somatic inactivation of *NKX3.1* in prostate cancer is reflected in decreased protein expression that is at first partial and then nearly complete at the time prostate cancer progresses to hormone-independence and metastatic disease (3, 4).

Loss of NKX3.1 expression is a very early event in prostate carcinogenesis. Gene targeting studies in mice showed that *Nkx3.1* haploinsufficiency alone can predispose to prostate epithelial dysplasia and can cooperate with other oncogenic mutations to augment prostate carcinogenesis (5, 6). Heterozygous *Nkx3.1*$^{+/-}$ mice have approximately 2/3 the Nkx3.1 protein levels of wild type mice. A similar reduction in NKX3.1 protein levels is seen in human prostatic intraepithelial neoplasia and in primary human prostate cancer (4). Not only is NKX3.1 down regulated in preinvasive prostate cancer, but NKX3.1 expression is reduced in regions of inflammatory atrophy that are precursors for malignant transformation (7). Inflammatory cytokines in these lesions can induce ubiquitination of NKX3.1 that targets the protein for degradation in the proteasome (8). Thus decreases in NKX3.1 can both predispose to and accompany prostate malignant transformation.

Although no somatic mutations of *NKX3.1* have been found in prostate cancer (9, 10), there are two well-characterized genetic variants associated with prostate cancer. A missense mutation was found that altered the N-terminal cap amino acid of the third, DNA-binding, helix in the homeodomain from a threonine to an alanine NKX3.1(T164A) that conferred risk for early prostate cancer in a family (11). Also we have described the *NKX3.1*(C154T) polymorphism now known as SNPrs2228013 that is found in approximately 10% of the population equally distributed among races and alters the coding

sequence for the protein (12). The missense mutation that changes arginine 52 to a cysteine affects propensity for phosphorylation at serine 48 and may affect protein function. Heterozygosity for this SNP has been suggested to be a risk factor for prostate cancer and is associated with prostatic enlargement (12, 13). The mechanism by which this genetic variant affects organ size or the occurrence of neoplasia is unknown.

Growth suppression by NKX3.1 is affected, in part, by inducing expression of insulin-like growth factor binding protein-3 (IGFBP-3), a known growth suppressor protein and down regulator of insulin-like growth factor-I (IGF-I) activity. IGF-I is a peptide growth factor that regulates cell growth, differentiation, and apoptosis by binding to the IGF receptor-I (IGFR-I) (14). IGFs are present in abundance in the circulation. Circulating IGF-I is bound mainly to IGFBP-3, one of the most abundant serum proteins (15). Although IGFBP-3 can inhibit the interaction of IGF-I with its receptor at the cellular level, serum IGFBP-3 also serves to stabilize circulating IGF-I (16). Serum levels of both proteins vary with age, nutrition, and hormonal status (17). Because of the effects of IGF-I on cell growth, survival, and apoptosis, the influence of both serum IGF-I and IGFBP-3 concentrations on cancer risk has been studied by a number of investigators (16). Serum IGF-I levels are associated with an elevated risk of prostate cancer in a variety of studies (18-26) that have been confirmed by meta analyses (27, 28). The risk that circulating IGF-I confers for prostate cancer may be related to its role as a growth and survival factor for prostate cancer cells (29-32). Here we show that NKX3.1(R52C) and a protein engineered for loss of the serine 48 phosphorylation site NKX3.1(S48A) do not activate expression of IGFBP-3. Consistent with this loss of function we hypothesize that the presence of the variant NKX3.1 protein may interact with circulating serum IGF-I to affect prostate cancer risk. Determination of *NKX3.1* genotype in two populations and analysis of serum IGF-I in the same study subjects is shown.

Materials and Methods

Cell Culture and Reagents The prostate cancer cell lines PC-3 and LNCaP, and the A172 human glioblastoma cell line were obtained from the American Type Culture Collection, Rockville, MD. PC-3 and A172 cell lines are grown in Modified IMEM (Invitrogen, Carlsbad, CA) containing 10% FBS. LNCaP cells are grown in Modified IMEM with phenol red (Invitrogen) containing 10% fetal bovine serum (FBS). PC-3 cells stably expressing the NKX3.1 expression vector are continuously grown in Modified IMEM (Invitrogen) containing 10% FBS and 1.2mg/ml G418 (Invitrogen). LNCaP cells were serum starved overnight in IMEM supplemented with 5% charcoal charcoal-stripped calf serum (CCS) and treated with 10nM R1881 for 48hr before harvesting.

Plasmids and Transfection Full length NKX3.1, NKX3.1(R52C), and NKX3.1(S48A) were expressed from constructs in the mammalian expression vector, pcDNA3.1 (Invitrogen) as previously described (33). Transient and stable transfections were carried out in 75 cm^2 cell culture flasks (Corning Inc., Corning, NY). Briefly, PC-3 and LNCaP prostate cancer cells were grown to 40-60% confluence and 4μg of plasmid DNA was transfected into the cell lines using Lipofectamine and Plus reagents (Invitrogen) in Opti-MEM (Invitrogen). After a 4hr incubation, the media was replaced with IMEM containing 10% FBS for an additional 24 hours. The PC-3 clones that stably express NKX3.1 were derived by transfection. After 4hr incubation in transfection reagent, PC-3 cells were trypsinized and seeded at a 1:30 density in Falcon Integrid 20 mm grid tissue culture dishes (Becton Dickinson, Franklin Lakes, NJ) in modified IMEM containing 10% FBS and 1.2mg/ml G418 (Invitrogen). The media was replaced every 4 days until colonies derived from a single cell could be seen with a light microscope. Individual colonies were isolated with sterile cloning disks (Scienceware, Pequannock, NJ) soaked in 0.25% Trypsin-EDTA

(Invitrogen) and grown to confluence in 6-well tissue culture dishes (Corning) for further study.

Western Blot Analysis. Cells were grown to 60-80% confluence and media was aspirated from the tissues culture dish. Immediately following media aspiration, lysis buffer was pipetted directly onto the cell monolayer and cells were scraped from the tissue culture flask. Cells were lysed with radioimmunoprecipitation assay (RIPA) buffer containing complete mini protease inhibitors (Roche, Nutley, NJ) and/or phosphatase inhibitors (Cell Signaling, Danvers, MA) followed by brief sonication to complete lysis. Sixty to ninety µg of total cell lysate was boiled in Novex® 2X Tris-glycine SDS sample buffer (Invitrogen) containing β-mercaptoethanol for six minutes and resolved on a 10-20% Tris-glycine SDS-PAGE gel (Invitrogen) Protein was then transferred onto a nitrocellulose membrane (Bio-Rad, Hercules, CA) and probed with primary antibody concentrations, as follows; β-actin (Sigma, St. Louis, MO) 1: 10,000; NKX3.1 (3) 1:2000; IGFBP-3 (sc-9028, Santa Cruz Biotechnology, Santa Cruz, CA) 1: 8,000 at 4°C overnight, followed by three washes in PBST. HRP conjugated goat-anti-rabbit and goat-anti-mouse (ImmunoPure® antibodies, Pierce Biotechnology, Rockford, IL) secondary antibodies in 1% milk or 1% BSA were applied for 1 hour at room temperature. Signal detection was performed with Super-Signal West Pico Chemiluminescent Substrate (Pierce Biotechnology).

Reverse Transcriptase PCR analysis Total RNA was extracted using the RNeasy Mini Kit (Qiagen) and cells were homogenized using the Qiashredder (Qiagen) method. 125-250ng of RNA was added to the RT-PCR master mix from One-step RT-PCR kit (Qiagen) (includes 5x buffer, DNTPs, and Taq polymerase). The following primers were used in the RT-PCR reactions: β-Actin (Fwd 5'-GGC CAC GGC TGC TTC-3' and Rev 5'-GTT GGC GTA CAG GTC TTT GC-3'); NKX3.1 (Fwd 5'-GCC GCA CGA GCA GCC AGA GAC A-3' and Rev 5'-TTC AGG GCC GGC AAA GAG GAG TG-3'); IGFBP-3 (Fwd 5'-CGC

CAG CTC CAG GAA ATG-3' and Rev 5'-GCA TGC CCT TTC TTG ATG ATG-3'); IGFBP-4 (Fwd 5'-TTA GCC CAA GAG GTC TGA GC-3' and Rev 5'-CTG TGC TTC AAG TCT TCC TTT G-3'); Lamin A/C (Fwd 5'-AAC TTC AGG ATG AGA TGC TGC G-3' and Rev 5'-GTC CAG AAG CTC CTG GTA CTC GT-3'). RT-PCR was performed in a Techne Techgene PCR machine; 30 min. at 50°; 15 min. at 94°; 22-30 cycles of 30s-1 min. at 94°, 30s-1 min. at melting temperatures of 55°-65°, and 30s-1 min. at 72°; followed by 15 min. at 72°. Samples were stored on ice until and mixed with 10x Blue Juice gel loading buffer (Invitrogen) and run on a 1.5% agarose gel containing 0.1μg/ml ethidium bromide in TAE buffer. Gels were imaged on a luminometer and recorded using a Kodak 1D digital camera.

IGF-IR Activation and Signaling. Cells were plated in 100mm culture dishes and washed twice with 1x phosphate buffered saline (PBS) before being serum starved for 14-16 hours in Modified IMEM containing 1.2mg/ml G418 (Invitrogen). Cells were then washed once with PBS and treated for 3 minutes with 100 pM IGF-I (a gift from Dr. J. Toretsky, Georgetown University, Washington, DC) in IMEM at 37°C. The media was immediately aspirated and cells were scraped from the flask and suspended in 2X Cell Lysis Buffer (Cell Signaling) containing phosphatase inhibitors and protease inhibitors by using Complete Mini tablets (Roche). Western blot analysis was completed as described above using anti-IGF-I-Rβ (#3027, Cell Signaling), anti-phospho-IGF-I Receptor(Tyr^{1131}) (#3021, Cell Signaling), anti-IRS-1 (06-248, Upstate), anti-phospho-IRS-1(Y^{612}) (44-816G, Biosource) primary antibodies. Bands were quantified by Scion Imager software and p-values were assessed from triplicate experiments by t-test analysis using Prism Graphpad software. [* indicates p-value of <0.05, ** indicates p-value of <0.005, *** indicates p-value of <0.001].

Cell Proliferation Assay PC-3 and derivative cell lines were seeded in triplicate in 96-well plates at a concentration of 4000 cells per well in IMEM containing 10% FBS (PC-3) or 10% FBS plus 1.2mg/ml G418 [PC-3(pcDNA3.1) and PC-3(NKX3.1)] and incubated for 24 hr at 37°C. At 24, 48, 72, and 96 hr after seeding, wells were trypsinized, suspended in IMEM, and immediately counted in a Beckman Coulter Z1 cell counter. Doubling times were calculated using Microsoft Excel and p-values were calculated by ANOVA.

Study Cohorts. Physicians Health Study: The participants of the Physicians Health Study (PHS) who comprised the prostate cancer cases and controls have been previously described in papers describing the effect of serum IGF-I (34) and *NKX3.1* genotype (12) on prostate cancer risk. The current analysis includes 937 cases and 1086 controls, using a prospective nested case-control design. Of the cases, 580 had Gleason score < 7, 334 had Gleason score >= 7 and 23 cases had unknown Gleason scores. Among the cases, 647 were T1/T2 and 197 were locally advanced or metastatic at presentation with the remaining 93 cases of unknown stage. Median age of cases at diagnosis was 70 years.

Risk Factors for Prostate Cancer Study: The Risk Factors for Prostate Cancer Study (RFPCS) is a population-based case-control study of prostate cancer in Australia. Prior approval of the study protocol was obtained from all relevant hospital and cancer registry human research ethics committees in Melbourne and Perth. Eligible cases comprised male residents of Melbourne and Perth diagnosed between 1994 and 1997 and recorded in the population-based cancer registries with a histopathology-confirmed diagnosis of adenocarcinoma of the prostate (International Classification of Diseases, 9th revision, rubric 185), excluding well-differentiated tumors (defined as low grade, *i.e.*, those with Gleason scores <5). Cases had to be <70 years of age at diagnosis. Controls were randomly selected from men on the current state electoral rolls and were frequency matched to the predicted age distribution of the cases in a ratio of one control per case. Potential controls

were matched against the cancer registries at the time of recruitment to exclude men with a known history of prostate cancer. Controls were identified and interviewed contemporaneously with the cases over the period 1994 to 1997. The cohort is comprised >95% of Caucasians. The lack of racial diversity is not critical to this analysis since the frequency of the *NKX3.1* polymorphism does not vary between races (12). A total of 798 cases and 527 controls were analyzed. Of the total cases 582 were described as low-to-moderate grade and 216 as high grade (Gleason score > 7 or poorly differentiated or undifferentiated tumors). Among the cases 545 were T1/T2 and 249 were locally advanced or metastatic at presentation with the remaining 4 cases of unknown stage. Median age for cases and controls was 62 years of age.

Serum IGF-I Assay. Serum IGF-I levels were determined by ELISA with reagents from Beckman Coulter (DSL, Webster, TX). All assays were performed in the laboratory of one of us (M.J.P.). Reliability of laboratory assays of plasma levels are always checked before measuring the real samples. The mean intra-pair coefficients of variation for blinded duplicate quality control samples were 2.6 % for IGF-I, and the long-term intra-person correlation coefficient for these biomarkers was 0.66 for IGF-I (3 years apart) (22). Cases and controls were separated by tertile of serum IGF-I levels. The median values for the IGF-I levels in the tertiles from the controls in each study are reported. For the PHS the IGF-I measurements were made at four different times when batches of 92, 257, 73, and 105 control samples were assayed. Batch-specific cut off points were used for tertiles and overall median values are reported as the mean of the three median values. Inclusion of the IGF-I values for the cases as well as controls changed the overall means by less than 1% for each tertile.

Statistical Analysis. For the PHS, the baseline characteristics and information at prostate cancer diagnosis for all the 937 cases and 1086 controls and for the subgroup of 673 cases

and 527 controls with both the genotype data and plasma IGF-I levels are presented in Table 1.

Using Pearson's goodness-of-fit test, the NKX3.1 SNP does not violated Hardy-Weinberg Equilibrium ($p>0.05$). Because of the low prevalence of the variant T allele, SNP was analyzed under a dominant model for both main effect analysis and the test of interactions. Cases and controls were matched by age and follow-up duration, but not by race. Because excluding non-Caucasians or conducting subgroup analysis led to losing some case-control pairs, we used an unconditional logistic regression model, to assess the risk of incident prostate cancer according to genotype, adjusting for the matching factors (age at randomization, smoking status, and follow-up time). We also conducted a subgroup analysis, comparing cases with Gleason score≥8 or clinically advanced stage (T3, T4, N1, or M1) to all controls.

We first conducted case-control analysis assessing the overall association of the NKX3.1 polymorphism with risk of developing prostate cancer among all the 937 cases and 1086 controls. We also evaluated the associations separately by Gleason grade (<7 vs. ≥7), by clinical stage (localized T1/T2 vs. advanced T3/T4/N1/M1), by fatal prostate cancer as outcome, and by year of the cancer diagnose (1982-1994 vs. 1997-2007) (Table 2). These analyses were then repeated by median age at diagnosis (<70 vs. ≥70 years). Finally, we assessed interaction between baseline plasma IGF-I levels and the NKX3.1 polymorphism (Table 5). We then assessed this interaction in the RFPC study using the same strategy. All statistics were calculated using SAS (version 9.1.3; SAS Institute Inc, Cary, NC), with a two-sided significance level of 0.05.

Results

NKX3.1(C154T) as a Risk Factor

Previously we had shown that among 1253 cases and controls in the PHS *NKX3.1*(C154T) (rs2228013) that codes for NKX3.1(R52C) was a mild risk factor for prostate cancer (12). We expanded this sample set to include cases from the PHS diagnosed more recently so that we now analyzed *NKX3.1* genotypes from 937 prostate cancer cases and 1086 age-matched controls. In this expanded sample set the *NKX3.1*(C154T) allele was related to prostate cancer risk to a similar degree as we had previously published (12) (Table 2). Importantly, among men with prostate cancer diagnosed before age 70, the median age at diagnosis in the PHS, rs2228013 was significantly associated with higher risk of overall prostate cancer (RR=1.55; 95% CI: 1.04-2.31), Gleason <7 (RR=1.71; 95% CI: 1.10-2.65), stage T1/T2 (RR=1.67; 95% CI: 1.09-2.57), and a higher risk of lethal cancer (metastatic cancer at diagnosis or fatal cancer during follow-up (RR=2.15; 95% CI: 1.00-4.63) (Table 3).

Effect of NKX3.1(R52C) on IGFBP-3 Expression and IGF-IR Activation

Amino acid 52 affected by rs2228013 is an arginine, located in a consensus motif that is a site for phosphorylation at serine 48. Replacement of arginine 52 with cysteine decreases phosphorylation at serine 48 by 70% (12). Thus a missense mutation at serine 48 potentially generates a protein with analogous, but more absolute, loss of serine 48 phosphorylation compared to NXK3.1(R52C). Expression of NKX3.1(R52C) in PC-3 cells induced substantially less *IGFBP-3* mRNA than did wild type NKX3.1 (Figure 1A). The mutant NKX3.1(S48A) protein was also attenuated in *IGFBP-3* induction, perhaps to a greater degree than NKX3.1(R52C) (Figure 1B). Western blotting confirmed that, as expected, neither NKX3.1(R52C) nor NKX3.1(S48A) induced IGFBP-3 protein expression in PC-3 cells (Figure 1C).

NKX3.1 expression attenuated IGFR-I activation in PC-3 cells via induced expression of IGFBP-3. The effect of NKX3.1 on IGFR-I activation was not seen when Long R-IGF-I, an IGFR-I ligand that does not bind to IGFBP-3 was used, or when cells were pretreated with *IGFBP-3* siRNA (35). In contrast, neither NKX3.1(R52C) nor NKX3.1(S48A) had an effect on IGFR-I signaling (Figures 2A and B). Moreover, signaling downstream from IGFR-I to IRS-1 is attenuated by NKX3.1 expression, but not by NKX3.1(R52C) or NKX3.1(S48A) (Figure 2C).

NKX3.1 suppresses cell proliferation in culture, an effect that is abrogated by siRNA to *IGFBP-3* (35). PC-3 cells have a doubling time of approximately 24 hrs that is extended to approximately 30 hrs by expression of NKX3.1. Neither NKX3.1(R52C) nor NKX3.1(S48A) affected PC-3 cell doubling time (Table 4) despite levels of NKX3.1 protein expression comparable to levels of wild type protein that suppressed proliferation (Supplementary Fig. 1).

Analysis of *NKX3.1* Genotype and Serum IGF-I

Since NKX3.1 regulates local IGFBP-3 expression in prostate and IGFBP-3 attenuates IGF-I signaling we asked whether *NKX3.1* genotype influenced the effect of IGF-I on prostate cancer risk. From participants in the Physicians' Health Study we analyzed 673 prostate cancer cases and 527 matched controls for which we were able to determine both *NKX3.1* genotype and serum levels of IGF-I (Table 5). The majority of cases (69%) in this cohort had been ascertained prior to 1994 and thus had been diagnosed prior to the widespread use of serum PSA for prostate cancer screening. Moreover, the blood samples were collected in 1982, prior to the diagnosis of prostate cancer in the cases. The frequency of rs2228013 among the control participants with IGF-I data was 6.83%, somewhat lower than the overall PHS controls (8.10%), and lower than the 11% we had originally found in our previous study (12). Table 5 shows the frequency of cases and

controls displayed by *NKX3.1* genotype and distributed across three tertiles of plasma IGF-I levels. Among participants homozygous for wild type *NKX3.1* there was no effect of plasma IGF-I on prostate cancer occurrence. However, among participants with *NKX3.1* variant T allele we found a 2.5-fold higher risk of prostate cancer comparing the highest to the lowest tertile of plasma IGF-I levels. The positive trend was apparent only among prostate cancer cases diagnosed before 1993, but not among cases diagnosed 1994 and after. *NKX3.1* genotype and serum IGF-I levels did not have a statistically significant interaction even among this subset probably due to the small sample size among T allele carriers (p for interaction = 0.2673).

We analyzed *NKX3.1* genotype and serum IGF-I in a second group of cases and controls from the RFPCS. These cases were diagnosed between 1994 and 1997 and are therefore considered largely screen-detected. The characteristics of this population are shown in the right column of Table 1. Noteworthy is that no prostate cancer cases with Gleason score < 5 were included in this cohort. In this population rs2228013 was present in 10.4% of the participants. These screened cases had a trend toward a younger age of diagnosis, lower stage distribution and lower grade distribution than the PHS cohort. Moreover, blood samples were drawn after the diagnosis of prostate cancer, not years prior as had been down with the PHS study samples. Among these participants there was no effect of *NKX3.1* genotype on prostate cancer risk. There was also no interaction with levels of serum IGF-I (Table 6). However, the effect of serum IGF-I levels alone on prostate cancer risk was seen in this population (Supplementary Table 1).

Discussion

NKX3.1 is important for prostate epithelial cell development, growth control, and differentiation (5, 36). Murine *Nkx3.1* is haploinsufficient and loss of a single allele manifests a phenotype similar to homozygous deletion, but with longer latency (5). In early

human prostate cancer we have found that NKX3.1 expression is down regulated over a broad range of expression levels with a median expression in primary prostate cancer of 0.67 the level in adjacent normal cells (4). In the course of determining the pathways of tumorigenesis that are affected by NKX3.1 we found that expression of IGFBP-3 in the prostate is downstream of NKX3.1 and that the effects of NKX3.1 on cell proliferation are mediated by IGFBP-3. In cultured cells NKX3.1 attenuates IGF-I signaling by activating IGFBP-3 expression (35). Importantly, *IGFBP-3* mRNA is among the genes most commonly down regulated in prostate cancer tissues compared to normal prostate tissues suggesting that its down regulation may play a role in prostate cancer pathogenesis (37).

NKX3.1 haploinsufficiency affects cell transformation, at least in part, by downstream effects on transcriptional targets. NKX3.1 binds to DNA and suppresses expression of genes downstream from cognate DNA binding sites (33). We have yet to identify a promoter that is transcriptionally activated by direct binding of NXK3.1 to its cognate DNA –TAAGTA- sequence. In fact, our experiments with reporter constructs containing NKX3.1 binding DNA suggested that NKX3.1 alone cannot initiate assembly of a transcriptional complex (33). NKX3.1 is known to interact with other transcription factors such as serum response factor (SRF) and serves as a synergistic co activator of promoters with serum response elements such as smooth muscle γ-actin (12, 38). Therefore the effect of NKX3.1 on gene expression is complex and is likely mediated by a number of cofactors. Because other NK homeodomain protein family members like Nkx2.5 interact with SRF, the physical interaction of NKX3.1 and SRF has been studied as a model for transcription factor interactions of NKX3.1. SRF is a widely expressed transcription factor involved in orchestrating disparate programs of gene expression linked to muscle differentiation and cellular growth (39). It is likely that different targets of transcriptional

activation are affected by the interaction of NKX3.1 with several different transcription factors.

We have shown an indirect link between NKX3.1 and transcription of IGFBP-3 mRNA. In cultured cells with NKX3.1 over expression we have shown a mechanistic link between NKX3.1, IGFBP-3 expression, IGF-IR activation, and cell proliferation. IGF1-R signaling is affected by many factors that regulate IGF-I availability and intracellular signaling downstream from the IGF-IR. Therefore, the interaction between NKX3.1 and IGFBP-3 expression in vivo is likely to be part a more complex system regulating the effect of IGF-I on prostate epithelial cells. The IGFBPs have functions that can compensate for one another making it difficult to determine specific functions of a single IGF binding protein by studies of gene-targeted mice (40, 41). Whether the same compensatory activation of IGF binding proteins occurs in prostate epithelial cell that have reduced NKX3.1 expression was not determined.

The presence of a variant *NKX3.1* allele was associated with prostate cancer risk in one prospective cohort but not in a second group of men assembled after the diagnosis of prostate cancer. Despite our observations from in vitro models that NKX3.1 blocks IGF-IR activation via IGFBP-3 we could not demonstrate a consistent interaction between *NKX3.1* genotype and circulating levels of IGF-I in the two study populations. *NKX3.1* genotype did affect Gleason score <7 tumors especially in men younger than 70. This observation is consistent with the notion that high-grade tumors are autonomous in their growth and less influenced by host factors, such as circulating IGF-I, or *NKX3.1* expression. In contrast, tumors with lower Gleason scores may have greater dependence on such factors. It is also worth noting the *NKX3.1* polymorphism was associated with an increased risk of lethal prostate cancer among those diagnosed prior to age 70.

Differences in the association between *NKX3.1* genotype and prostate cancer risk in the two studies we analyzed may be due to the effect of over diagnosis of prostate cancer. The Physicians Health Study population includes a large fraction of cases diagnosed prior to mid-1990 and therefore prior to the adoption of widespread PSA screening for prostate cancer. On the other hand, the Risk Factors for Prostate Cancer Study includes only cases diagnosed between 1994 and 1997. Histologic foci of prostate cancer are concomitants of aging and are found in all men. PSA screening is a highly sensitive test that has caused an increase in the total number of cases diagnosed each year contributing to a substantial over diagnosis. Some estimates identify as many as 42% or more of all cases as over diagnosed (42). Thus many cases diagnosed during the PSA era may be biologically different from the bulk of those diagnosed before the adoption of screening on a large scale, when most diagnosed cases were clinically meaningful and carried a more serious prognosis. Ours is not the only study to find disparate results between case-control groups from the pre- and post-PSA screening era and it is likely that PSA screening has altered the biology that is being analyzed in large case studies collected after the mid 1990s (43, 44).

The PHS and RFPCS also differed in the timing of blood collection that was used for serum IGF-I determinations. The PHS group was a nested case control study, with prospectively collected samples. IGF-I levels were determine on samples collected before the diagnosis of cancer. In contrast, for the RFPCS case-control study, the blood was collected after diagnosis and perhaps after treatment had been initiated. Thus, in the case-control setting, one is always concerned that either the disease, or treatment, or both could affect the blood levels.

Down regulation of NKX3.1 protein per se is sufficient to predispose cells to malignant transformation. In addition we have described a family in which hereditary prostate cancer cosegregated with a T164A missense mutation in the NKX3.1

homeodomain that reduced DNA binding by 95% (11). Haploinsufficiency is a reflection of the dominant nature of regulation by NK family members. Both missense and truncation mutations in NKX2.5 are autosomal dominant determinants of congenital cardiac abnormalities (45, 46). Similarly, mutations in NKX2.1/TTF cause pulmonary and thyroid developmental abnormalities (47). Paradoxically, *NKX2.1* is amplified in a subset of lung cancers and NKX2.1 over expression contributes to cell transformation and oncogenesis (48). We argue that tumor suppression by NKX3.1 is exerted in a relative manner by modulation of downstream targets to different degrees. Our finding that IGFBP-3 expression in human prostate cancer cells correlates quantitatively with NKX3.1 expression levels is reminiscent of findings that *Nkx3.1* gene dosage determines the degree of transcriptional effects in gene targeted mice (49). Analysis of downstream targets of *Nkx3.1* identified a number of genes related to differentiation, but did not identify *Igfbp-3* (50). We, on the other hand, showed that prostatic *Igfbp-3* mRNA levels correlate with *Nkx3.1* gene copy number in gene-targeted mice (35). Further studies will identify additional NKX3.1 targets and elucidate their role in prostate cancer suppression and, perhaps, prevention.

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Table 1

Characteristics of Two Study Populations

		PHS - overall (%)	PHS with IGF-I (%)	RFPCS (%)
Participants		2023	1200	1325
Cases		937	673	798
	Dx prior to 1994	532(57)	465(69.09)	0
	Dx after 1994	405(43)	208(30.91)	798
Age at Diagnosis				
	<55	21(2.24)	17(2.53)	110 (13.8)
	55-64	258(27.53)	204(30.31)	421 (52.7)
	65-69	242(25.83)	169(25.11)	267 (33.5)
	70-74	221(23.59)	160(23.77)	
	≥ 75	195(20.81)	123(18.28)	
Stage				
	T1/T2	647(69.05)	461(68.50)	545 (68.3)
	T3/T4	150(16.01)	114(16.94)	249 (31.2)
	N1/M1	47(5.02)	39(5.79)	
	Missing	93(9.93)	59 (8.77)	4 (0.5)
Grade				
	Gleason<7 Low/Med Grade	580(61.90)	414(61.52)	582 (72.9)[1]
	Gleason≥7, High Grade	334(35.64)	239 (35.51)	216 (27.1)
	Missing	23(2.45)	20(2.97)	
NKX3.1 **codon 154**	C/C	844	604	719 (90.1)
	C/T or T/T	93(9.92)	69 (10.25)	79 (9.9)
IGF-I (ng/ml)	Tertile 1		133.7[2]	52.3
	Tertile 2		186.4	68.0
	Tertile 3		243.7	86.4

[1]All cases with Gleason score < 5 were excluded.
[2]For details on calculation see Materials and Methods.

Table 2

Odds ratios of Prostate Cancer by NKX3.1 Genotype in the PHS

	Genotype	Case (n)	Case (%)	Control (n)	Control (%)	Odds ratio
Overall	C C	844	90.1	998	91.9	1.00
	C T	91	9.7	84	7.7	
	T T	2	0.2	4	0.4	
	C T/T T	93	9.9	88	8.1	1.25 (0.92-1.71)
Dx 1982-1993	C C	481	90.4	998	91.9	1.00
	C T/T T	51	9.6	88	8.1	1.21 (0.83-1.77)
Dx 1994-2007	C C	363	89.6	998	91.9	1.00
	C T/T T	42	10.4	88	8.1	1.22 (0.77-1.94)

Table 3

Odds ratios of Prostate Cancer by NKX3.1 Genotype Among Men With Age<70 yrs at Diagnosis: results from the PHS

	Genotype	Cases	(%)	Controls	(%)	Odds ratio
Overall	C C	460	88.3	564	92.2	1.00
	C T/T T	61	11.7	48	7.8	1.55 (1.04-2.31)
Gleason<7	C C	296	86.8	564	92.2	1.00
	C T/T T	45	13.2	48	7.8	1.71 (1.10-2.65)
Gleason≥7	C C	156	91.2	564	92.2	1.00
	C T/T T	15	8.8	48	7.8	1.14 (0.62-2.10)
Stage T1/T2	C C	324	87.3	564	92.2	1.00
	C T/T T	47	12.7	48	7.8	1.67 (1.09-2.57)
Stage T3/T4/N1/M1	C C	110	91.7	564	92.2	1.00
	C T/T T	10	8.3	48	7.8	1.12 (0.54-2.29)
Metastatic or fatal prostate cancer	C C	62	86.1	564	92.2	1.00
	C T/T T	10	13.9	48	7.8	2.15 (1.00-4.63)
Year of diagnosis 1982-1993	C C	259	90.2	564	92.2	1.00
	C T/T T	28	9.8	48	7.8	1.30 (0.78-2.19)
Year of diagnosis 1994-2007	C C	201	85.9	564	92.2	1.00
	C T/T T	33	14.1	48	7.8	1.80 (1.03-3.15)

Table 4
Effect of NKX3.1 Expression on Cell Proliferation

Cell Type	Doubling Time	p-value
PC-3	25.34 ± 1.91	0.1716
PC-3(Control)	24.26 ± 2.05	*
PC-3(NKX3.1)-1	32.24 ± 5.91	0.0037
PC-3(NKX3.1)-2	38.88 ± 7.82	0.0002
PC-3(NKX3.1)-8	30.24 ± 2.55	0.002
PC-3(NKX3.1)(S48A)-25	22.19 ± 1.31	0.1368
PC-3(NKX3.1)(S48A)-27	22.94 ± 0.98	0.3221
PC-3(NKX3.1)(S48A)-28	22.42 ± 2.00	0.2053
PC-3(NKX3.1(R52C)-1	24.34 ± 1.50	0.9555
PC-3(NKX3.1)(R52C)-26	25.94 ± 1.48	0.2264
PC-3(NKX3.1)(R52C)-27	26.41 ± 1.69	0.1357

The cell doubling time, in hours, of parental PC-3 cells, PC-3(pcDNA3.1) cells, and PC-3(NKX3.1) clones was assayed by cell counting. Cells were counted at 24, 48, 72, and 96 hours post-seeding and doubling times were calculated. In the lower section of the table PC-3(pcDNA3.1) and PC-3(NKX3.1)-1 cells were treated with transfection reagent alone, the missense siRNA oligonucleotide, and the IGFBP-3 siRNA oligonucleotide for 24 hours before the first cell count was taken. p-values were calculated in comparison to the PC-3(pcDNA3.1) cell doubling time, using ANOVA. NS = not significant.

Table 5

Odds ratios of Prostate Cancer by NKX3.1 Genotype and IGF-I Level in the Physicians Health Study

Genotype	IGF-I tertile	Case/ Control	Odds ratio*	p-interaction
Overall: CC	1	197/ 162	1.00 (ref)	0.24
	2	203/ 166	1.029 (0.77-1.38)	
	3	204/ 163	1.07 (0.79-1.45)	
C/T or T/T	1	12/ 12	0.82 (0.36-1.87)	
	2	25/ 11	1.93 (0.92-4.05)	
	3	32/ 13	2.04 (1.03-4.04)	
Dx 1982-1993: CC	1	135/ 162	1.00 (ref.)	0.27
	2	144/ 166	1.23 (0.87-1.73)	
	3	140/ 163	1.31 (0.92-1.85)	
C/T or T/T	1	9/ 12	0.98 (0.38-2.55)	
	2	14/ 11	1.63 (0.70-3.83)	
	3	23/ 13	2.49 (1.16-5.32)	
Dx 1994-2007: CC	1	62/ 162	1.00 (ref)	0.57
	2	59/ 166	0.56 (0.34-0.93)	
	3	64/ 163	0.69 (0.42-1.14)	
C/T or T/T	1	3/ 12	0.39 (0.09-1.65)	
	2	11/ 11	2.68 (0.96-7.52)	
	3	9/ 13	0.92 (0.31-2.75)	

* Adjusted for baseline age, smoking status, and follow-up duration.

Table 6. NKX3.1 Genotype and Serum IGF-I Levels in Risk Factors for Prostate Cancer Study Participants

Genotype	IGF-I (teriles)	Case/ Control	Odds ratio*	p-interaction
Overall: CC	T1	216/161	1.00 (ref)	0.18
	T2	200/153	0.97 (0.72 - 1.33)	
	T3	303/154	1.39 (1.04 - 1.87)	
C/T or T/T	T1	25/22	0.76 (0.40 - 1.44)	
	T2	30/17	1.39 (0.72 - 2.69)	
	T3	24/20	0.86 (0.44 - 1.64)	

Figure Legends

Figure 1. The effect of NKX3.1 variant proteins on IGFBP-3 expression in PC-3 cell clones. A and B. RT-PCR analysis of 250ng total mRNA isolated from PC-3 cell clones. A172 is a positive control for IGFBP-3 mRNA expression and LNCaP is a positive control for NKX3.1 mRNA expression. C. Western blot analysis of 60μg whole cell lysate from PC-3(pcDNA3.1), PC-3(NKX3.1), PC-3(NKX3.1 R52C), and PC-3(NKX3.1 S48A) cell clones. A172 cell line was used as a positive control for IGFBP-3 protein expression.

Figure 2. The effect of NKX3.1 variant proteins on IGF-IR activation in PC-3 cells. A. Western blot analysis of 90μg of total protein extracted from PC-3(pcDNA3.1) and PC-3(NKX3.1)(R52C) stable cell clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. B. Western blot analysis of 90μg of total protein extracted from PC-3(pcDNA3.1) and PC-3(NKX3.1)(S48A) stable cell clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. C. Western blot analysis of 90 μg of total protein extracted from PC-3(pcDNA3.1), PC-3(NKX3.1)-1, PC-3(NKX3.1)(R52C)-1, and PC-3(NKX3.1)(S48A)-28 clones that were serum starved for 16 hours and treated with 100pM IGF-I. The values in the graph are the means from three separate experiments. A representative western blot is shown in the inset. * indicates a value different from the PC-3(pcDNA3.1) control with a $p<0.001$.

Supplementary Figure 1. Expression of NKX3.1 in derivative PC-3 cell clones. Panels from western blots of β-actin and NKX3.1 are shown from exponentially growing cultured cells from which equal amounts of total protein were loaded onto a gel. Numbers indicate

identities of i ndividual independently d erived c lones. A c ell e xtract f rom P C-3 cel ls transfected with the empty vector is shown at the far left as a negative control.

Supplementary Table 1 : Serum IGF-I Levels and Prostate Cancer Risk in Risk Factors for Prostate Cancer Study Participants

Log (IGF-I) (Quantiles)	Case/Controls	OR (95% CI)	P-value[2]	P-het[3]
1st quantile	173/130			0.04
2nd quantile	171/134	1.01 (0.72 to 1.41)	0.963	
3rd quantile	176/123	1.10 (0.78 to 1.54)	0.590	
4th quantile	278/140	1.48 (1.07 to 2.03)	0.016	

Log (IGF-I) (Tertiles)	Case/Controls	OR (95% CI)	P-value[2]	P-het[3]
1st Tertile	241/183			0.05
2nd Tertile	230/170	1.05 (0.78 to 1.40)	0.76	
3rd Tertile	327/174	1.37 (1.04 to 1.81)	0.025	

Log (IGF-I) (Median)	Case/Controls	OR (95% CI)	P-value[2]	P-het[3]
< Median	344/264			0.03
≥ Median	454/263	1.30 (1.03 to 1.63)	0.028	

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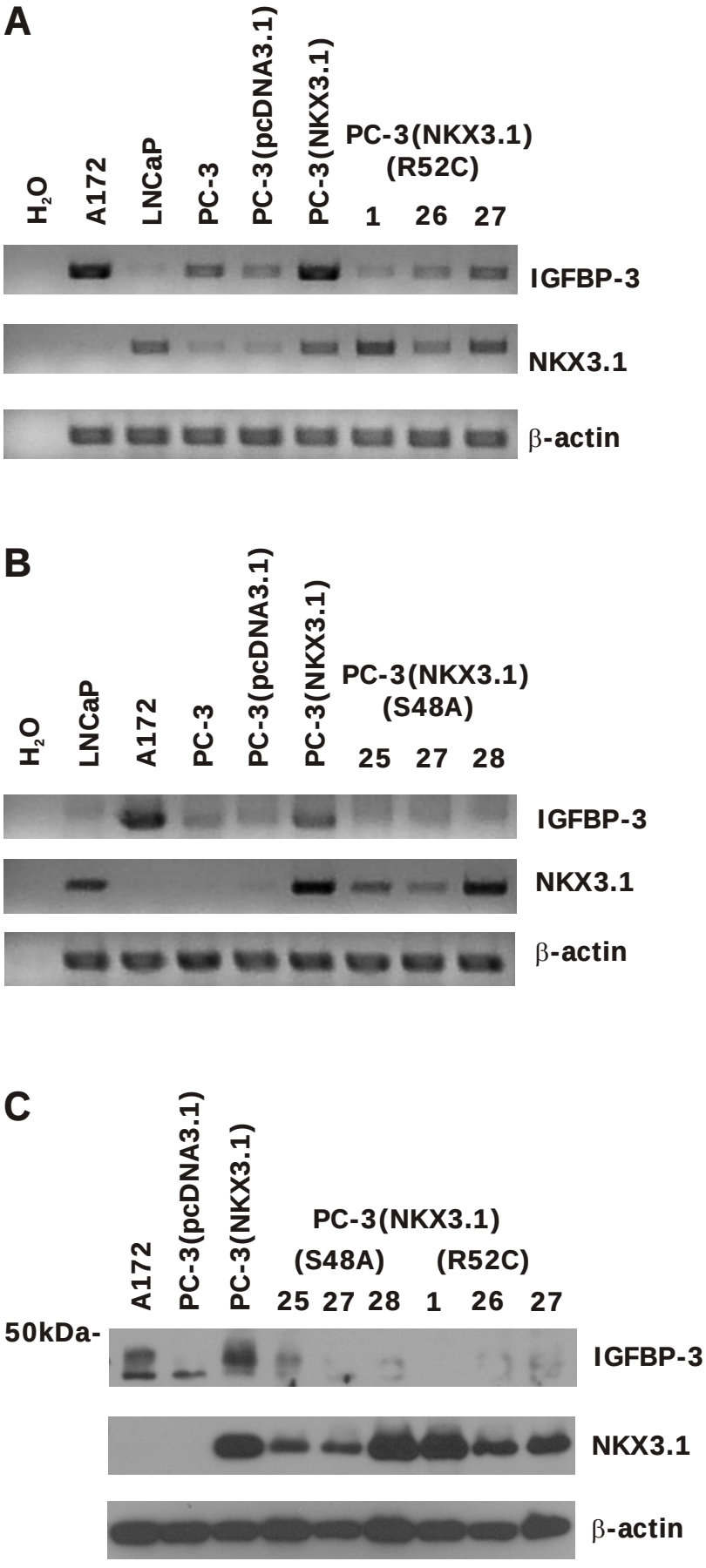

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Fig 1

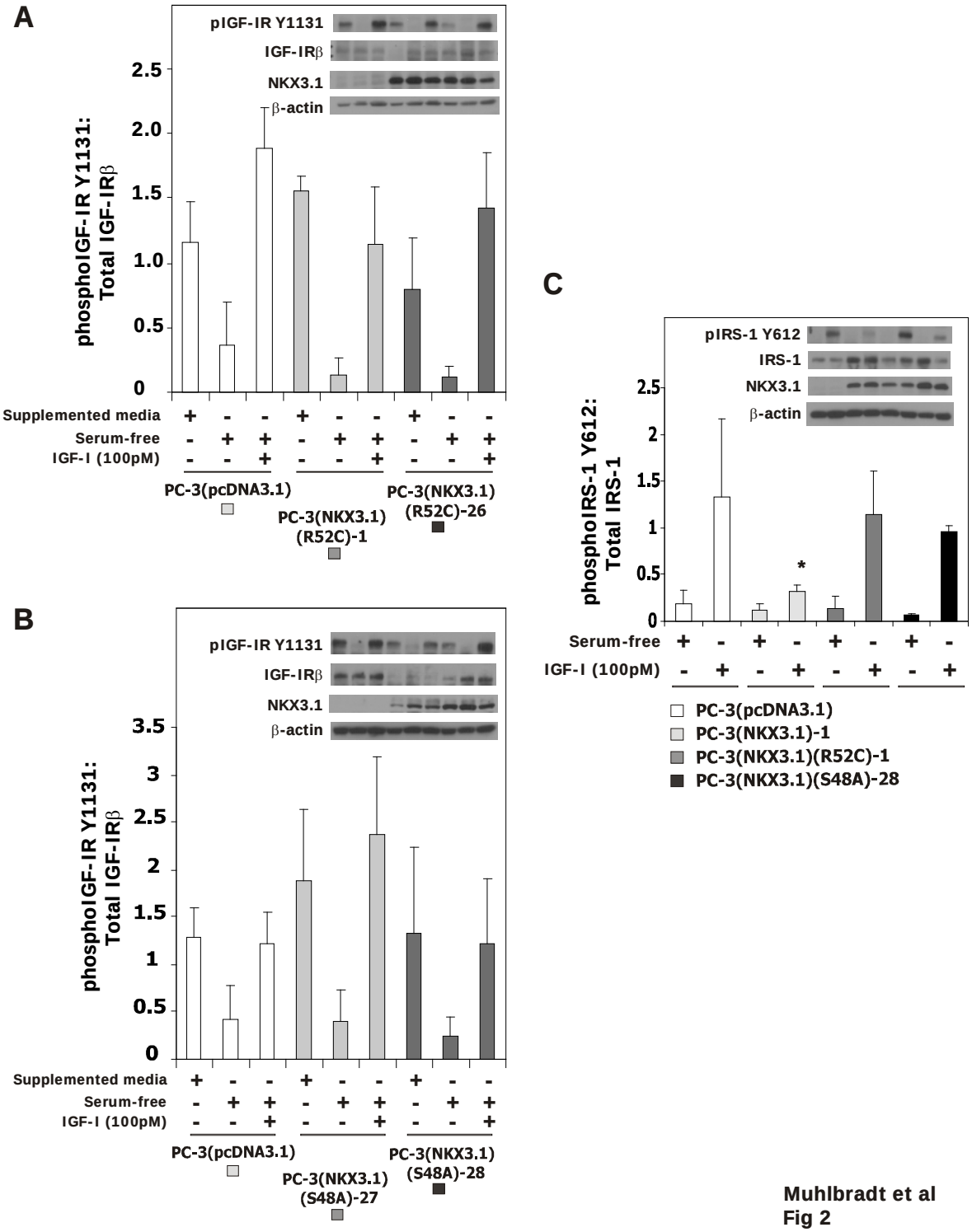

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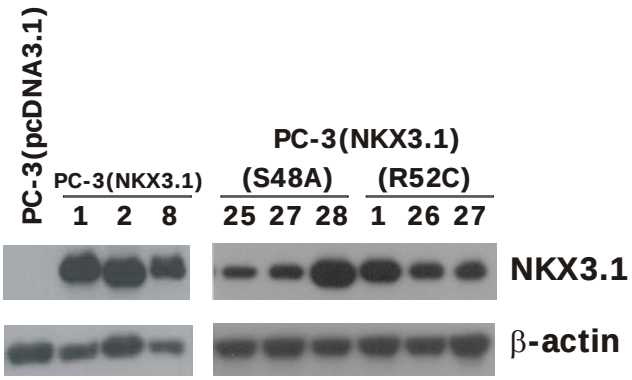
Fig 2



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Supplementary Fig 1